

GenCore version 5.1.6
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tein search, using sw model

March 18, 2004, 13:24:49 ; Search time 21 seconds
(without alignments)

1067.268 Million cell updates/sec

US-09-909-005-1
1170

1 MLKPSVTSAPTADWATLVTV.....LLLIQQQQQQQQQQTQNHMS 233

BLOSUM62

Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues

hits satisfying chosen parameters: 283366

ength: 0

ength: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

% Match	Query Length	DB	ID	Description
56.6	317	2	T27179	hypothetical prote
20.0	1131	2	T15617	hypothetical prote
18.7	852	2	T10811	channel associated
18.6	870	2	G01974	channel associated
17.8	960	1	A39651	discs-large tumor
16.8	720	2	A45436	synapse-associated
16.8	724	2	JH0800	postsynaptic densi
16.8	767	2	T09599	postsynaptic densi
16.4	904	2	I38757	homolog of brosopt
16.4	911	2	I56552	synapse-associated
16.4	926	2	I38756	homolog of Drosoph
16.4	2055	2	T30259	multiple PDZ domai
15.9	2054	2	T46612	multi PDZ domain p
15.1	1012	2	T23160	hypothetical prote
15.0	431	2	T16191	hypothetical prote
14.8	2450	2	S71625	protein-tyrosine-p
14.7	2466	2	I67629	protein-tyrosine-p
14.4	2294	2	I67630	protein-tyrosine-p
14.3	117	2	I81209	tyrosine phosphata
14.3	126	2	I81210	tyrosine phosphata
14.1	1171	2	T42372	probable guanylate
14.1	1256	2	J50209	brain-specific ang
14.1	2490	1	A54971	protein-tyrosine-p
13.8	1337	2	T13948	atypical protein k
13.6	578	2	T21345	hypothetical prote
13.2	390	2	T28036	hypothetical prote
13.2	423	2	T21570	hypothetical prote
13.2	440	2	T21568	hypothetical prote
12.9	538	2	I59291	beta1-syntrophin -

30 151 12.9 628 2 T09458 numb-bind
31 151 12.9 728 2 T09457 numb-bind
32 151 12.9 1112 2 T32733 AMPA glut
33 151 12.9 1277 2 T14152 synaptic
34 150.5 12.9 87 2 S60315 PSD-95-re
35 147.5 12.6 488 2 I51379 syntrophin
36 147.5 12.6 488 2 I51379 syntrophin
37 146.5 12.5 503 2 I84771 alpha-syn
38 145.5 12.4 505 2 S62894 syntrophin
39 145.5 12.4 1893 2 A56158 eye devel
40 144.5 12.4 450 2 G01158 tyrosine
41 144.5 12.4 1281 2 T00346 hypotheti
42 142.5 12.2 358 2 I46532 protein c
43 140.5 12.0 1095 2 T43275 neurabin
44 138.5 11.8 2172 2 T20145 hypotheti
45 137.5 11.8 624 2 T19630 hypotheti

ALIGNMENTS

RESULT 1

T27179

hypothetical protein Y54G11A.10 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-C

C:Accession: T27179

R:Wallis, J.

submitted to the EMBL Data Library, December 1998

A:Reference number: Z20322

A:Accession: T27179

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-317 <WIL>

A:Cross-references: EMBL:AL034488; NID:e1359895; PIDN:CAA22459.1; CF

A:Experimental source: clone Y54G11A

C:Genetics:

A:Gene: CESP:Y54G11A.10

A:Introns: 55/3; 108/3; 175/3; 228/2; 253/3

Query Match 56.6%; Score 662; DB 2; Length 317;
Best Local Similarity 68.4%; Pred. No. 2.5e-42;
Matches 130; Conservative 30; Mismatches 30; Indels 0;

QY 25 LRDVARAIELLEKLGESVPHKLOSLKKVLQSEFCTAIRVYQVMHETITV
DB 117 LERDVRILELMEHVQKTGEVNNAKLASLQVLOSEFFGAVREVYETVYESIDA
QY 85 RARATKATVAAPAAASEGSHSRVVELPKTDEGLGPNVNGKQNSPIYISRII
DB 177 KAATAKATVAAPAAAEAGHAHPRIVELPKTDQGLGPNVNGKQNSPIYISRII
QY 145 RHGGLKRGDQLLSVNGSVSEGEHHEKAVELLKAAKDSVKLVYRTPKVLREMEZ
DB 237 RHGGLKRGDQLLIAGVNVVAECHEKAVDLLKSAVGVSKLVIRYMPKLLDEMEF
QY 205 TARRRQQQQL 214
DB 297 IRSTQQSQPTL 306

RESULT 2

T15617

hypothetical protein C25P6.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-S

C:Accession: T15617

R:Bentley, D.

submitted to the EMBL Data Library, October 1995

A:Description: The sequence of C. elegans cosmid C25P6.

A:Reference number: Z18377

A:Accession: T15617

A:Status: preliminary; translated from GB/EMBL/DDBJ

C:Genetics:

A:Gene: chapsyn-110

C:Superfamily: discs-large tumor suppressor; GLGF domain homology; g

F:198-276/Domain: GLGF domain homology <GLG2>

F:543-601/Domain: SH3 homology <SH3>

F:681-858/Domain: guanylate kinase homology <GKI>

Query Match 18.6%; Score 217.5; DB 2; Length 870;

Best Local Similarity 29.3%; Pred. No. 1.7e-08;

Matches 55; Conservative 31; Mismatches 59; Indels 43;

QY 43 GRVPVHKLSKKVLQSFCTAIRVYQVMHFTITVNGCFEFRARATAKATVA

DB 385 GLLPDSMTS-----HSQSHSTATQPSMTLQRAVSLG-----

QY 103 HSHPRVVELPKTDEGLGFNGWGWGKEQNSPIYISRIIPGVVAERHGLKEGDQLLA

DB 418 --EPRKVVVLHKGSTGLGFNI VGG-EDGEGLFVSFILAAGPADLSGELQRGDGLL

QY 163 VSEGEHHEKAVELLKAAKQSVKLVVRYTPKVLSEMEAREPEKLR

DB 475 LRASHEQAALAKGAGVTIIAQYQPEDYARPEAKTHDLREQVMHNSMSGSGS

QY 210 QQQQLLIQ 217

DB 535 QKRSLYVR 542

RESULT 5

A39631

discs-large tumor suppressor - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 10-Sep-1999 #revision_revise 10-Sep-1999 #text_change 10-S-

C:Accession: A39651

R:Woods, D.F.; Bryant, P.J.

Cell 66, 451-464, 1991

A:Title: The discs-large tumor suppressor gene of Drosophila encodes

A:Reference number: A39651; MUID:91330294; PMID:1651169

A:Accession: A39651

A:Molecule type: mRNA

A:Residues: 1-960 <WOO>

A:Cross-references: GB:W73529; NID:q157243; PTDN:AAA28468.1; PID:q15

C:Comment: Loss of this protein causes large imaginal disks by allow

tion to control cellular proliferation.

C:Genetics:

A:Gene: FlyBase:dlg1

A:Cross-references: FlyBase:FBgn001624

C:Superfamily: discs-large tumor suppressor; GLGF domain homology; g

C:Keywords: signal transduction

F:45-123/Domain: GLGF domain homology <GLG1>

F:159-241/Domain: GLGF domain homology <GLG2>

F:491-563/Domain: GLGF domain homology <GLG3>

F:607-665/Domain: SH3 homology <SH3>

F:771-948/Domain: guanylate kinase homology <GKI>

Query Match 17.8%; Score 208.5; DB 1; Length 960;

Best Local Similarity 39.3%; Pred. No. 9e-08;

Matches 46; Conservative 21; Mismatches 49; Indels 1;

QY 88 ATAKATVAAPAAEGSHSHPRVVELPKTDEGLGFNGWGWGKEQNSPIYISRIIPGG

DB 466 AVPPGTPRAVSTEDITREPRITTIQKPGQGLGFNI VGG-EDGQGIYVSPFLAGG

QY 148 GLKRGDQLLSVNGSVGEHHEKAVELLKAAKQSVKLIVRYTPKVLSEMEAREPE

DB 525 ELKRGDQLLSVNNVNLTHATHEAAQAKTSGGVVTLAQVRRPEEYNRRFEARQ

RESULT 6

A54336

synapse-associated protein SAP90 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 22-Sep-1993 #revision revision 18-Nov-1994 #text_change 21-J-

136 anzel, B.M.; Veh, R.W.; Cases-Langhoff, C.; Garner, A.M.; Appeltauer, U.
58, 4580-4583, 1993
a rat presynaptic protein related to the product of the Drosophila tumor
ar: A45436; MUID:93186749; PMID:7680343
136
inary; not compared with conceptual translation
nucleic acid
J <KIS>
ource: brain
extracted from NCBI backbone (NCBIP:126555)
iscs-large tumor suppressor; GLGF domain homology; guanylate kinase hom
: GLGF domain homology <GLG1>
: SH3 homology <SH3>
: guanylate kinase homology <GKI>
16.8%; Score 196.5; DB 2; Length 720;
ilarity 41.4%; Pred. No. 5e-07;
Conservative 19; Mismatches 38; Indels 1; Gaps 1;
VVELPKTDEGLGFNVWGKQNSPIYISRIIPGVAERHGGKRGDQLLSVNGVSVG 165
RIVHRGSTGLGFNVGG-EDGEGIFISFILAGGPADLSGELRGDQLLSVNGVDLRN 369
HEKAVELKAAKDSVKLVVRYTPKVLMEARFEKLR 204
HEQAALAKNAGQVTIIAQYKPEYSRFEAKIHDLR 408

sity protein PSD-95 - rat
s: brain specific PSD-95 protein; discs-large tumor suppressor protein h
s norvegicus (Norway rat)
993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
800; S26407
t, C.A.; Kennedy, M.B.
2, 1992
brain postsynaptic density fraction contains a homolog of the drosophil
er: JH0800; MUID:93040233; PMID:1419001
800
mRNA
4 <CHO>
es: GB:M96853; NID:G206454; PIDN:AAA41971.1; PID:G206455
ource: brain
iscs-large tumor suppressor; GLGF domain homology; guanylate kinase hom
: GLGF domain homology <GLG1>
: SH3 homology <SH3>
: guanylate kinase homology <GKI>
16.8%; Score 196.5; DB 2; Length 724;
ilarity 41.4%; Pred. No. 5.1e-07;
Conservative 19; Mismatches 38; Indels 1; Gaps 1;
VVELPKTDEGLGFNVWGKQNSPIYISRIIPGVAERHGGKRGDQLLSVNGVSVG 165
RIVHRGSTGLGFNVGG-EDGEGIFISFILAGGPADLSGELRGDQLLSVNGVDLRN 369
HEKAVELKAAKDSVKLVVRYTPKVLMEARFEKLR 204
HEQAALAKNAGQVTIIAQYKPEYSRFEAKIHDLR 408

usity protein 95 - human
sapiens (man)
999 #sequence_revision 16-Jul-1999 #text_change 21-Jan-2000
1599
.; Hoover, K.H.; You, Z.; Bryant, P.J.
; EMBL Data Library, July 1998

A;Reference number: Z16761
A;Accession: T09599
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-767 <STA>
A;Cross-references: EMBL:U83192; NID:G3318652; PID:G3318653
A;Experimental source: mammary
C;Genetics:
A;Gene: PSD95
C;Superfamily: discs-large tumor suppressor; GLGF domain homology; 9
F:208-286/Domain: GLGF domain homology <GLG>
F:478-536/Domain: SH3 homology <SH3>
F:578-755/Domain: guanylate kinase homology <GKI>

Query Match 16.8%; Score 196.5; DB 2; Length 767;
Best Local Similarity 41.4%; Pred. No. 5.4e-07;
Matches 41; Conservative 19; Mismatches 38; Indels 1;
QY 106 PRVELPKTDEGLGFNVWGKQNSPIYISRIIPGVAERHGGKRGDQLLSVN
Db 354 PRRIIVHRGSTGLGFNVGG-EDGEGIFISFILAGGPADLSGELRGDQLLSVN
QY 166 EHHEKAVELKAAKDSVKLVVRYTPKVLMEARFEKLR 204
Db 413 ASHEQAALAKNAGQVTIIAQYKPEYSRFEAKIHDLR 451

RESULT 9
I38757
homolog of Drosophila discs large protein, isoform 1 - human
C;Species: Homo sapiens (man)
C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 21-J
C;Accession: I38757
R;Lue, R.A.; Marfatia, S.M.; Branton, D.; Chishti, A.H.
Proc. Natl. Acad. Sci. U.S.A. 91, 9818-9822, 1994.
A;Title: Cloning and characterization of hdlg: the human homologue c
A;Reference number: I38756; MUID:95024052; PMID:7937897
A;Accession: I38757
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-904 <RES>
A;Cross-references: EMBL:U13897; NID:G558437; PIDN:AAA50599.1; PID:G
C;Genetics:
A;Gene: GDB:DIG1
A;Cross-references: GDB:393278; OMIM:601014
A;Map position: 3q29-3q29
C;Superfamily: discs-large tumor suppressor; GLGF domain homology; 9
C;Keywords: alternative splicing; duplication
F:229-307/Domain: GLGF domain homology <GLG1>
F:324-402/Domain: GLGF domain homology <GLG2>
F:588-646/Domain: SH3 homology <SH3>
F:715-892/Domain: guanylate kinase homology <GKI>

Query Match 16.4%; Score 192; DB 2; Length 904;
Best Local Similarity 35.2%; Pred. No. 1.4e-06;
Matches 44; Conservative 23; Mismatches 44; Indels 14;
QY 106 PRVELPKTDEGLGFNVWGKQNSPIYISRIIPGVAERHGGKRGDQLLSVN
Db 464 PRKVLVHRGSTGLGFNVGG-EDGEGIFISFILAGGPADLSGELRGDQLLSVN
QY 166 EHHEKAVELKAAKDSVKLVVRYTPKVLMEARFEKLR-----T7
Db 523 ASHEQAALAKNAGQVTIIAQYKPEYSRFEAKIHDLRQWMNNSISSGSGSI
QY 213 QLLIQ 217
Db 583 SLVVR 587

RESULT 10
I56552
synapse-associated protein 97 - rat

```
3 norvegicus (Norway rat)
396 #sequence_revision 26-Jul-1996 #text_change 21-Jan-2000
352
Kistner, U.; Veh, R.W.; Cases-Langhoff, C.; Becker, B.; Gundelfinger, E.
ar characterization and spatial distribution of SAP97, a novel presynap
ar: I56552; MUID:95198112; PMID:7891172
352
inary; translated from GB/EMBL/DBJ
mRNA
1 <RES>
98: EMBL:U14950; NID:g642455; PIDN:AAA79976.1; PID:g642456
iscs-large tumor suppressor; GLGF domain homology; guanylate kinase hom
: GLGF domain homology <GLG1>
: GLGF domain homology <GLG2>
: SH3 homology <SH3>
: guanylate kinase homology <GKI>
16.4%; Score 192; DB 2; Length 911;
ilarity 35.2%; Pred. No. 1.5e-06;
Conservative 23; Mismatches 44; Indels 14; Gaps 2;
VVELPKTDEGLGNVWGKEQNSPIYISRIIPGVAERHGLKRGDQLLSVNGSVSVEG 165
KVLHRSSTGLGNVIGG-EDGEGIFSFILAGPADLSGELRKGDRRIISVNSVDLRA 521
HEKAVELLKAAKDSVKLVVRYTPKVLMEARFEKLR-----TARRRQQQ 212
HEQAAALKAGQAVTIQAQYRPEYRFEAKIHLDRQMNSVSSGSGSLRTSQKR 581
JFQ 217
FVR 586

phila discs large protein, isoform 2 - human
sepiens (man)
956 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000
756
fatia, S.M.; Branton, D.; Chishti, A.H.
. Sci. U.S.A. 91, 9818-9822, 1994
ar: I38756; MUID:95024052; PMID:7937897
756
inary
mRNA
6 <RES>
98: EMBL:U13896; NID:g558435; PIDN:AAA50598.1; PID:g558436
98: GDB:393278; OMIM:601014
3q29-3q29
iscs-large tumor suppressor; GLGF domain homology; guanylate kinase hom
native splicing; duplication
: GLGF domain homology <GLG1>
: GLGF domain homology <GLG2>
: SH3 homology <SH3>
: guanylate kinase homology <GKI>
16.4%; Score 192; DB 2; Length 926;
ilarity 35.2%; Pred. No. 1.5e-06;
Conservative 23; Mismatches 44; Indels 14; Gaps 2;
VVELPKTDEGLGNVWGKEQNSPIYISRIIPGVAERHGLKRGDQLLSVNGSVSVEG 165
KVLHRSSTGLGNVIGG-EDGEGIFSFILAGPADLSGELRKGDRRIISVNSVDLRA 522
HEKAVELLKAAKDSVKLVVRYTPKVLMEARFEKLR-----TARRRQQQ 212
HEQAAALKAGQAVTIQAQYRPEYRFEAKIHLDRQMNSVSSGSGSLRTSQKR 582
```

QY 213 QLLIQ 217
DB 583 SLVYR 587

RESULT 12
T30259
multiple PDZ domain protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-J
C:Accession: T30259
R:Simpson, B.H.; Suffolk, R.; Jackson, I.J.
Genomics 59, 102-104, 1999
A>Title: Identification, sequence, and mapping of mouse multiple PDZ
A:Reference number: 220797; MUID:99326529; PMID:10395806
A:Accession: T30259
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2055 <SIM>
A:Cross-references: EMBL:AJ131869; NID:g4150877; PIDN:CAA10523.1; PI
A:Experimental source: strain C57/BL6 X CBA F1; whole brain
C:Genetics:
A:Gene: mpdz
A:Map position: 4

Query Match 16.4%; Score 191.5; DB 2; Length 2055;
Best Local Similarity 29.0%; Pred. No. 4.2e-06;
Matches 56; Conservative 31; Mismatches 81; Indels 25;

QY 1 MLKPSVTSAPTADMAT---LTVVQPLTLDRVARAIELLEKLOESGSEVPVHKL
DB 1879 MMHENGVAATQKLRVGDRIIVICGTSTGDMTHTQAVNLKMNAGSIEVQVVAG

QY 57 LQSEFCTAIREVQYMHETITVNGCEPRARATAKATVAAPFAASEGSHPRVVE
DB 1939 TG-----HQEELANFLAP---TGLTSSIFPPDDLGPSSQSKTIT

QY 117 GLGFNVWGG---KEQNSPIYISRIIPGVAERHGLKRGDQLLSVNGSVSVEGEH
DB 1981 GLSFNVGGVSGSHGDLPIYKTVFAKGAAGDGLKEGDQITAVNGQSLEGVT

QY 174 LLKAAKDSVKLVV 186
DB 2041 ILKRTKGTVTLMV 2053

RESULT 13
T46612
multi PDZ domain protein 1 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-J
C:Accession: T46612
R:Ullmer, C.; Schmuck, K.; Figge, A.; Lubbert, H.
FEBS Lett. 424, 63-68, 1998
A>Title: Cloning and characterization of MUPP1, a novel PDZ domain p
A:Reference number: 223104; MUID:98196865; PMID:9537516
A:Accession: T46612
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2054 <ULL>
A:Cross-references: EMBL:AJ001320; NID:g2959978; PIDN:CAA04681.1; PI
A:Experimental source: brain
C:Genetics:
A:Gene: MUPP1

Query Match 15.9%; Score 186.5; DB 2; Length 2054;
Best Local Similarity 28.5%; Pred. No. 9.9e-06;
Matches 55; Conservative 31; Mismatches 82; Indels 25;

QY 1 MLKPSVTSAPTADMAT---LTVVQPLTLDRVARAIELLEKLOESGSEVPVHKL
DB 1878 MMHENGVAATQKLRVGDRIIVICGTSTGDMTHTQAVNLKMNAGSIEVQVVAG

us-09-909-005-1.rpr

Matches	45;	Conservative	26;	Mismatches	46;	Indels	14;
Qy	107	RVVELPKTDEGLGFNTWGGKE--QNSPTIYSRIIPGVAERHGKLRGGDQLLSV	:	:	:	:	:
Dd	36	QVVIVKKPDSFGSLSGGSSENAQMNVISKFKGLPADECSELFIQDAIVEV	:	:	:	:	:
Qy	165	GEHHEKAVELJKAOKSVKLVVRY-----TP-----KVLE---EMEARFEKLRITA	:	:	:	:	:
Dd	96	GQSHDEVNMLKSSGGQVTLVGVYRTHMTFLPKPAQSLQDPDTLDDQLDFGRSTF	:	:	:	:	:
Qy	213	QLLIQQQQQQQ 223	:	:	:	:	:
Dd	156	EESRLSDSKWQQ 166	:	:	:	:	:

Search completed: March 18, 2004, 13:28:52
Job time : 21 secs

Query	Match	Length	DB	ID	Description
§	18.7	852	1	DLG2_RAT	Q63622 rattus norv
	18.6	870	1	DLG2_HUMAN	Q57800 homo sapien
	17.8	960	1	DLG1_DROME	PL1007 drosophila
	17.4	817	1	DLG3_HUMAN	Q92796 homo sapien
	17.4	849	1	DLG3_MOUSE	P70175 mus musculu
	17.4	849	1	DLG3_RAT	Q62936 rattus norv
	16.8	724	1	DLG4_MOUSE	Q62108 mus musculu
	16.8	724	1	DLG4_RAT	P10316 rattus norv
	16.8	767	1	DLG4_HUMAN	P78332 homo sapien
	16.4	904	1	DLG1_HUMAN	Q12959 homo sapien
	16.4	911	1	DLG1_RAT	Q62696 rattus norv
	14.4	2485	1	PTND_HUMAN	Q12923 homo sapien
	14.3	1356	1	PAD3_HUMAN	Q8tew0 homo sapien
	13.8	1333	1	PAD3_MOUSE	Q99nh2 mus musculu
	13.8	1337	1	PAD3_RAT	Q92340 rattus norv
	13.7	540	1	SNB2_HUMAN	Q13425 homo sapien
	13.5	520	1	SNB2_MOUSE	Q61235 mus musculu
	13.5	537	1	SNB1_MOUSE	Q99188 mus musculu
	13.5	637	1	MP34_HUMAN	Q96j38 homo sapien
	13.5	206	1	SJZB_RAT	Q9wv74 rattus norv
	13.4	539	1	STG2_HUMAN	Q9ny39 homo sapien
	13.2	631	1	IL16_HUMAN	Q14005 homo sapien
	13.2	631	1	IL16_PANTR	Q62666 pan troglod
	13.0	145	1	SJZB_HUMAN	P57105 homo sapien
	13.0	910	1	US1C_MOUSE	Q9es44 mus musculu
	12.9	538	1	SNB1_HUMAN	Q13884 homo sapien
	12.9	728	1	LNK1_MOUSE	Q70263 mus musculu
	12.9	1275	1	AIPI1_MOUSE	Q9wv91 mus musculu
12.9	1277	1	AIPI1_RAT	Q88382 rattus norv	
12.9	1455	1	AIPI1_HUMAN	Q86ul8 homo sapien	
12.6	539	1	STG2_MOUSE	Q92560 mus musculu	
12.6	728	1	LNK1_HUMAN	Q9tbb1 homo sapien	
12.6	505	1	SNB1_RABIT	Q28626 oryctolagus	

```

RN 0001478; PDZ.
RP SEQUENCE FROM N.A.
RX MEDLINE=96310881; PubMed=8755482;
RA Kim E., Cho K.-O., Rothschild A., Sheng M.;
RT "Heteromultimerization and NMDA receptor-clustering activity of
RT Chapsyn-110, a member of the PSD-95 family of proteins.";
RL Neuron 17:103-113 (1996).
CC -!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF NMDA RECEPTOR
CC SUBUNITS AS WELL AS POTASSIUM CHANNELS.
CC -!- SIMILARITY: Belongs to the MAGUK family.
CC -!- SIMILARITY: Contains 3 PDZ/DHR domains.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -!- SIMILARITY: Contains 1 guanylate kinase-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a cc
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CC -----
DR EMBL; U32376; AB04949.1; -.
DR PIR; G01974; G01974.
DR HSSP; Q12959; 1PDR.
DR Genew; HGNC:2901; DLG2.
DR MIM; 603583; -.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0004385; F:guanylate kinase activity; TAS.
DR InterPro; IPR008144; Guanylate_kin.
DR InterPro; IPR008145; Guanylt/Ca.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00625; Guanylate_kin; 1.
DR Pfam; PF00595; PDZ; 3.
DR Pfam; PF00018; SH3; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00072; GuK; 1.
DR SMART; SM00228; PDZ; 3.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
DR PROSITE; PS00502; GUANYLATE_KINASE_2; 1.
DR PROSITE; PS0106; PDZ; 3.
DR PROSITE; PS00002; SH3; 1.
KW SH3 domain; Repeat.
FT DOMAIN 98 184 PDZ 1.
FT DOMAIN 193 279 PDZ 2.
FT DOMAIN 421 501 PDZ 3.
FT DOMAIN 536 606 SH3.
FT DOMAIN 680 870 GUANYLATE KINASE.
SQ SEQUENCE 870 AA; 97500 MW; 89C83BA0619F6F59 CRC64;

Query Match 18.6%; Score 217.5; DB 1; Length 870;
Best Local Similarity 29.3%; Pred.No.2.9e-08;
Matches 55; Conservative 31; Mismatches 59; Indels 43;

QY 43 GEVPEKQLSLKVLQSEFCTAIREVYQYMHETITVNGCPFRARATAKATVAJ
Db 385 GLLPSEMTS-----HSQSTATQPSMTLQRAVSLEG-----
QY 103 HSHPRVLPKTDGLGFNWMGKEQNSPIYISRIIPGVVAERHGLKRGDQLI
Db 418 --EPRKVLVHLKSGTGLGFNIVGG-EDGEGIFVSVILAGGADLSGELQDQII
QY 163 VEGEHKAVELLKAAKDSVKLVVRYTPKVLMEARFEKLK-----
Db 475 LRASHEQAAALKGAGQVTIIAQYQPDYARFEAKIHDLREOMHMSSE
QY 210 QQOQLLIQ 217
Db 535 QKRSUYVR 542

```

STANDARD; PRT; 960 AA.

(Rel. 26, Created)
 (Rel. 26, Last sequence update)
 (Rel. 42, Last annotation update)
 -1 tumor suppressor protein.
 DLG1.
 melanogaster (Fruit fly).
 Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Adopterygota; Diptera; Brachycera; Muscomorpha;
 Drosophilidae; Drosophila.
 7227;

DM N.A., AND FUNCTION.

FO;

30294; PubMed=1651169;

Bryant P.J.;

large tumor suppressor gene of Drosophila encodes a
 inase homolog localized at septate junctions.;

-464(1991).

N: Plays a critical role at septate junctions in cellular
 control during larval development. The presence of a
 e kinase domain suggests involvement in cellular adhesion
 as signal transduction to control cellular proliferation.
 a for maintenance of cell polarity.

JULAR LOCATION: CYTOSKELETON-ASSOCIATED. LOCATED AT THE
 SMIC FACE OF THE MEMBRANE IN THE CELLULAR BLASTODERM AND
 ASSOCIATED WITH SEPTATE JUNCTIONS WHICH BEGIN TO FORM
 EPITHELIAL CELLS AT THE TIME OF DORSAL CLOSURE. IN ADULT
 LOCATED AT THE APICAL-LATERAL MEMBRANE BOUNDARY OF
 IAL CELLS.

TIVE PRODUCTS:

lternative splicing; Named isoforms=1;

at=A number of isoforms are produced;

=P31007-1; Sequence=Displayed;

SPECIFICITY: In embryos, expression is seen in epithelial
 and some nervous tissue. In larvae, expression is seen as a
 ound salivary glands and imaginal disks, also in
 rculus and parts of the brain. Expressed in adult
 ctive tissues.

MENTAL STAGE: Expressed both maternally and zygotically

out development.

ITY: Belongs to the MAGUK family.

ITY: Contains 3 PDZ/DHR domains.

ITY: Contains 1 SH3 domain.

ITY: Contains 1 guanylate kinase-like domain.

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 n Bioinformatics Institute. There are no restrictions on its
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 d this statement is not removed. Usage by and for commercial
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 email to license@isb-sib.ch).

9; AAA28468.1; -.

; A39651.

6; 1BFE.

gn0001624; dlgl.

179; C:apical cortex; IDA.

327; C:apicolateral plasma membrane; IDA.

946; C:septate junction; NAS.

175; P:basal protein localization; IMP.

391; P:dorsal closure; NAS.

197; P:establishment and/or maintenance of epithel. . .; NAS.

334; P:establishment and/or maintenance of polarit. . .; IGI.

336; P:establishment and/or maintenance of polarit. . .; NAS.

399; P:neurogenesis; IMP.

273; P:regulation of synapse; IMP.

PR008144; Guanylate_kin.

DR InterPro; IPR008145; Guanylt/Ca.
 DR InterPro; IPR001478; PDZ.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00625; Guanylate_kin; 1.
 DR Pfam; PF00595; PDZ; 3.
 DR Pfam; PF00018; SH3; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00072; GuKc; 1.
 DR SMART; SM00228; PDZ; 3.
 DR SMART; SM00336; SH3; 1.
 DR PROSITE; PS00856; GUANYLATE KINASE_1; 1.
 DR PROSITE; PS00052; GUANYLATE KINASE_2; 1.
 DR PROSITE; PS0106; PDZ; 3.
 DR PROSITE; PS00002; SH3; 1.
 KW Transducer; SH3 domain; Alternative splicing; Repeat.
 FT DOMAIN 40 126 PDZ 1.
 FT DOMAIN 154 244 PDZ 2.
 FT DOMAIN 486 566 PDZ 3.
 FT DOMAIN 600 670 SH3.
 FT DOMAIN 768 960 GUANYLATE KINASE.
 SQ SEQUENCE 960 AA; 102468 MW; BF87A4262F1B6AD5 CRC64;

Query Match 17.8%; Score 208.5; DB 1; Length 960;

Best Local Similarity 39.3%; Pred. No. 1.4e-07;

Matches 46; Conservative 21; Mismatches 49; Indels 1;

QY 88 ATAKATVAATFAAEGSHSRVVELPKDEGLGFNVMGKQNSPIYISRIIPGG
 DB 466 AVPTPTFANSTEDITREPRITITKQPGQLGNIVGG-EDGQGIYVSFILAGG
 QY 148 GLKRGDQLLSNVGVSVEGHEKAVELLKAADSVKLIVRYTPKVLSEMEARPE
 DB 525 ELKRGDQLLSNVNVLNTHATHEAAQALKTSGGVVTLAQRPEEYNRFEARIQ

RESULT 4

DLG3 HUMAN STANDARD; PRT; 817 AA.
 ID DLG3 HUMAN Q9ULI8;
 AC Q92736; Q9ULI8;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Presynaptic protein SAP102 (Synapse-associated protein 102)
 DE (Neuroendocrine-DLG) (NE-DLG) (Disce, large homolog 3).
 GN DLG3 OR KIAA1232.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Petal brain;
 RX MEDLINE=97332623; PubMed=9188857;
 RA Makino K., Kawahara H., Masuko N., Nishiyama Y., Morisaki T.,
 RA Sasaki J., Nakano M., Kuwano A., Nakata M., Ushio Y., Saya H.;
 RT "Cloning and characterization of NE-dlg: a novel human homolog
 RT Drosophila discs large (dlg) tumor suppressor protein interacts
 RT the APC protein.";
 RL Oncogene 14:2425-2433 (1997).
 RN [2]
 RP SEQUENCE OF 330-817 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20039619; PubMed=10574462;
 RA Nagase T., Ishikawa K.-I., Kikuno R., Hirose M., Nomura N.,
 RA Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes
 RT The complete sequences of 100 new cDNA clones from brain which
 RT for large proteins in vitro.";
 RL DNA Res. 6:337-345 (1999).
 CC -!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMDA R
 CC -!- SUBUNIT NP2B (BY SIMILARITY).
 CC -!- SIMILARITY: Belongs to the MAGUK family.
 CC -!- SIMILARITY: Contains 3 PDZ/DHR domains.


```

[1]
RN      SEQUENCE FROM N.A.
RP      STRAIN=C57BL/6; TISSUE=Brain;
RC      Kohnmueller N., Makino S., Yagi T.;
RR      Submitted (Aug-1996) to the EMBL/GenBank/DBST databases.
RL      RBL
CC      -1- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NM2D A
CC      SUBUNIT NR2B.
CC      -1- SIMILARITY: Belongs to the MAGUK family.
CC      -1- SIMILARITY: Contains 3 PDZ/DHR domains.
CC      -1- SIMILARITY: Contains 1 SH3 domain.
CC      -1- SIMILARITY: Contains 1 guanylate kinase-like domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a co
CC      between the Swiss Institute of Bioinformatics and the EMBL o
CC      the European Bioinformatics Institute. There are no restricti
CC      use by non-profit institutions as long as its content is
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CC      entities requires a license agreement (See http://www.isb-sib.ch)
CC      or send an email to license@isb-sib.ch.

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EMBL; D87117; BAAL3249.1; -.
DR
DR
DR HSP; Q12959; IPRF.
DR
DR MG; MG1:188986; Digh3.
DR
DR GO; GO:0005737; C:Cytoplasm; IDA.
DR
DR GO; GO:0005515; F:protein binding; IPI.
DR
DR InterPro; IPRC08144; Guanylate_kin.
DR
DR InterPro; IPRC08145; Guanylt/Ca.
DR
DR InterPro; IPRC01478; PDZ.
DR
DR InterPro; IPRC01452; SH3.
DR
DR Pfam; PF00625; Guanylate_kin; 1.
DR
DR Pfam; PF00595; PDZ; 3.
DR
DR Pfam; PF00018; SH3; 1.
DR
DR ProDom; PD000066; SH3; 1.
DR
DR SWAP; SW00073; Cys2; 1.
DR

DR	SWAK; SM000728; GUAC; 1.
DR	SWAR; SM002826; PDZ; 3.
DR	SWAT; SM003346; SH3; 1.
DR	PROSITE; PS00856; GUANYLATE KINASE 1; 1.
DR	PROSITE; PS00102; GUANYLATE KINASE 2; 1.
DR	PROSITE; PS50052; GUANYLATE KINASE 2; 1.
DR	PROSITE; PS50106; PDZ; 3.
DR	PROSITE; PS50002; SH3; 1.
KW	SH3 domain; Repeat.
FT	DOMAIN 149 235
FT	DOMAIN 244 330
PDZ	PDZ 2.
PDZ	PDZ 3.
FT	DOMAIN 404 484
FT	DOMAIN 519 589
SH3	SH3

SEQ	DOMAIN	559	849	GUNARYLATE KINASE
SEQUENCE	849 AA;	53482 MW;	EF34F2D7513538EE	CRC64;
Query Match		17.4%;	Score 203.5;	DB 1;
Best Local Similarity		43.4%;	Pred. No. 2.8e-07;	Length 849;
Matches	43;	Conservative 18;	Mismatches 37;	Indels 1;
Qy	106	PRVVELPKTDEGLGNFNVWGKGEQNSPIYISRIIPGVGAERHGGIKRGDOLLVN		
Ddb	402	PRKILKHGKSTGLGNFNVWG-EDGEGIFVSFIAGGADSLSGELRRGDRILVN		
Ov	166	RHEPKAVELLKAAKTSVKIVVRYTPKVIEMAREFEKIR 204		

RESULT 6	1D	DIG3 RAT	1D	DIG3 RAT	STANDARD;	PRT;	849 AA.
AC	QG2936;	P70547;					
AC	01-NOV-1997	(Rel. 35, Created)					
EDT	01-NOV-1997	(Rel. 35, Last sequence update)					
EDT	10-OCT-2003	(Rel. 42, Last annotation update)					
EDT	Presynaptic protein SAPI02	(Synapse-associated protein 102) (PS					
EDT	95/SAP90 related protein 1)	(Discs, large homolog 3).					
EDT	DIG3.	DIG3.					
EDT	Rattus norvegicus	(Rat).					
EDT	Rukavotora	Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi					

utheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
10116;

OM N.A. (ISOFORM LONG).

74358; PubMed=8780649;
L., Kistner U., Kindler S., Chung W.J., Kuhlendahl S.,
L., Lau L.-F., Veh R.W., Haganir R.L., Gundelfinger E.D.,
novel postsynaptic protein that interacts with NMDA
complexes in vivo.;
55-265(1996).

OM N.A. (ISOFORM SHORT).

ta Y., Takai Y.;
SEP-1996) to the EMBL/GenBank/DBJ databases.
N: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMDA RECEPTOR
NR2B.

ITVE PRODUCTS:

alternative splicing; Named isoforms=2;

ng;
i=Q62936-1; Sequence=Displayed;

ort;
i=Q62936-2; Sequence=VSP 003151;

ITY: Belongs to the MAGUK family.

ITY: Contains 3 PDZ/DHR domains.

ITY: Contains 1 SH3 domain.

ITY: Contains 1 guanylate kinase-like domain.

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email to license@isb-sib.ch).

7; AAA93031.1; -

7; AAB48561.1; -

9; 1PDR.

PRO08144; Guanylate_kin.

PRO08145; Guanylt/Ca.

PRO01478; PDZ.

PRO01452; SH3.

25; Guanylate_kin; 1.

95; PDZ; 3.

18; SH3; 1.

100066; SH3; 1.

1072; GuK; 1.

1228; PDZ; 3.

326; SH3; 1.

100856; GUANYLATE_KINASE_1; 1.

150052; GUANYLATE_KINASE_2; 1.

150106; PDZ; 3.

150002; SH3; 1.

Repeat; Alternative splicing.

149 235 PDZ 1.

244 330 PDZ 2.

404 484 PDZ 3.

519 589 SH3.

659 849 GUANYLATE_KINASE.

627 640 Missing (in isoform Short).

/FTid=VSP 003151.

849 AA; 93539 MW; 34DA9C46C7BB96DB CRC64;

ilarity 17.4%; Score 203.5; DB 1; Length 849;

Conservative 18; Mismatches 37; Indels 1; Gaps 1;

RVLEPKTDEGLGVNMGKEQNSPIYISRIIPGGVAERHGLKRGDQLISGVNVSVEG 165

KXILHKGSTGLGVNIVGG-EDGEGIFV8FILLAGGPADL8GELRRGDRILL8VNGVNLRN 460

QY 166 EHHEKAVELLKAAKDSYKLVVRYTPKVLNEMEARFEKLR 204
Db 461 ATHEQAAALKRAGOSVTIVAQYRPEEYSRFSKIHDLR 499

RESULT 7

DLG4 MOUSE

ID DLG4 MOUSE STANDARD; PRT; 724 AA.

AC Q62108;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Presynaptic density protein 95 (PSD-95) (Presynaptic protein 95)

GN DLG4 OR DLGH4 OR PSD95.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostor

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M

OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.

RC STRAIN=DBA/2; TISSUE=Brain;

RA Kohmura N., Yagi T.;

RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Interacts with the cytoplasmic tail of NMDA recep

CC subunits. May be involved in synaptogenesis.

CC -!- SUBUNIT: Interacts with DLGAP1/GKAP and with KCND2 (By

CC or SHANK3 (By similarity). Interacts through its third PDZ

CC with NLGN1, and probably with NLGN2 and NLGN3. Interacts th

CC its first PDZ domain with GRK2, KCNA4 and CRIPT. Interacts

CC through its second PDZ domain with NOS1 and CAPON (By simi

CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Concentrated at synaptic

CC junctions primarily on the presynaptic side. Also found in

CC postsynaptic density of neuronal cells (By similarity).

CC -!- SIMILARITY: Belongs to the MAGUK family.

CC -!- SIMILARITY: Contains 3 PDZ/DHR domains.

CC -!- SIMILARITY: Contains 1 SH3 domain.

CC -!- SIMILARITY: Contains 1 guanylate kinase-like domain.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; D50621; BAA09297.1; -

DR HSP; P31016; 1BE9.

DR MGD; MGI:1277959; Dlg4.

DR InterPro; IPR008144; Guanylate_kin.

DR InterPro; IPR008145; Guanylt/Ca.

DR InterPro; IPR001478; PDZ.

DR InterPro; IPR001452; SH3.

DR Pfam; PF00625; Guanylate_kin; 1.

DR Pfam; PF00595; PDZ; 3.

DR Pfam; PF00018; SH3; 1.

DR ProDom; PD000066; SH3; 1.

DR SMART; SM00072; GuK; 1.

DR SMART; SM00228; PDZ; 3.

DR SMART; SM00326; SH3; 1.

DR PROSITE; PS00856; GUANYLATE_KINASE_1; 1.

DR PROSITE; PS50052; GUANYLATE_KINASE_2; 1.

DR PROSITE; PSS0106; PDZ; 3.

DR PROSITE; PSS0002; SH3; 1.

KW SH3 domain; Repeat.

FT DOMAIN 65 151 PDZ 1.

FT DOMAIN 160 246 PDZ 2.

FT DOMAIN 313 393 PDZ 3.

FT DOMAIN 428 498 SH3.

FT DOMAIN 534 724 GUANYLATE_KINASE.

SEQUENCE 724 AA; 80472 MW; 7EFFC99E1FF90BA CRC64;

[illegible]

us-09-909-005-1.rsp

[illegible]

DE Presynaptic protein SAP97 (Synapse-associated protein 97) (Disc.
DE large homolog 1).
GN DLAG

```
0; AAA79976.1; -.
      ; I56552.
8; IPDR.
PR008144; Guanylate kin.
PR008145; Guanylt/Ca.
PR004172; L27..
PR001478; PDZ.
PR001452; SH3.
25; Guanylate_kin; 1.
95; PDZ; 3.
18; SH3; 1.
00066; SH3; 1.
072; GuKc; 1.
589; L27; 1.
228; PDZ; 3.
326; SH3; 1.
00856; GUANYLATE KINASE_1; 1.
50052; GUANYLATE_KINASE_2; 1.
50106; PDZ; 3.
50002; SH3; 1.
Repeat.
224 310 PDZ 1.
318 404 PDZ 2.
465 545 PDZ 3.
580 650 SH3..
721 911 GUANYLATE KINASE.
527 530 POLY-ALA.
911 AA; 100570 MW; 18CEBD31DDCAFB8 CRC64;
16.4%; Score 192; DB 1; Length 911;
ilarity 35.2%; Pred.No. 2.le-06;
Conservative 23; Mismatches 44; Indels 14; Gaps 2;
VVELPKTDEGLGNWVGKEQNSPIYISRIIPGGVAERHCGIKRGDQLLSVNGSVGE 165
```

R.L., Feingold E.A., Grouse L.H., Derge J.G., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Marusina K., Farmer A.A., Rubin G.M., Hong L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Telon E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., W., Touchman J.W., Green E.D., Dickson M.C., C.C., Grimwood J., Schmutz J., Myers R.M., Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Schein J.E., Jones S.J.M., Marra M.A.; and initial analysis of more than 15,000 full-length human DNA sequences." Acad. Sci. U.S.A. 99:16899-16903 (2002).

WITH TRIP6.
29089; PubMed=10400701;
Clark K., Fortin Y., Shen S.-H., Barville D.;
Yin-related protein, interacts with the second PDZ domain
solic protein tyrosine phosphatase hPTP1E.";
em. 274:20679-20687 (1999).

WITH NGFR.
12928; PubMed=10544233;
Chiya T., Rabizadeh S., Maruyama W., Mukai J., Li Y.,
Bredesen D.E., Sato T.A.;
Interaction of Fas-associated phosphatase-1 (FAP-1) with
d their effect on NF-kappaB activation.";
460:191-198 (1999).

Y NMR OF 1361-1456 UNCOMPLEXED AND IN COMPLEX WITH THE
OF TNFRSF6.
70882; PubMed=10704206;
Gehring K., Ekiel I.;
Structure of the PDZ2 domain from human phosphatase hPTP1E
interactions with C-terminal peptides from the Fas
Y 39:2572-2580 (2000).

Y NMR OF 1361-1456 IN COMPLEX WITH THE C-TERMINUS OF THE
LEUCIDE EXCHANGE FACTOR RA-GEF-2.
90786; PubMed=12095257;
Banville D., Gehring K., Ekiel I.;
Structure of the PDZ2 domain from cytosolic human
hPTP1E complexed with a peptide reveals contribution of
eak3 loop to PDZ domain-ligand interactions.";
1. 320:813-820 (2002).

O-1419 AND MET-1522.
23362; PubMed=12436199;
Harada H., Nagai H., Fukino K., Teramoto A., Emi M.;
Ad juxtaposition of Fas-associated phosphatase-1 (FAP-1)
H2-terminal kinase 3 (JNK3) genes: genomic structure and
orphisms of the FAP-1 gene.";
et. 47:614-619 (2002).

N: Regulates negatively Fas-induced apoptosis and NGFR-
pro-apoptotic signaling.
IC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
e + phosphate.
: Interacts with TRIP6 and TNFRSF6 (Fas receptor) through
and PDZ domain. Interacts with the C-terminal SVP motif of
rough its third PDZ domain.
UAR LOCATION: Cytoplasmic (By similarity).
TIVE PRODUCTS:
Alternative splicing; Named isoforms=4;
=Q12923-1; Sequence=Displayed;

Names=2;
IsoId=Q12923-2; Sequence=VSP_000496;
Names=3;
IsoId=Q12923-3; Sequence=VSP_000497;
Names=4;
IsoId=Q12923-4; Sequence=VSP_007921;
Note-May be due to a competing donor splice site;
-!- TISSUE SPECIFICITY: Present in most tissues with the except
the liver and skeletal muscle. Most abundant in lung, kidney
fecal brain.
CC -!- SIMILARITY: Contains 1 FERM domain.
CC -!- SIMILARITY: Contains 5 PDZ/DHR domains.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase fan
Non-receptor class subfamily.
CC
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EMBL; U12128; AAB60339.1; -
EMBL; D21209; BAA04750.1; -
EMBL; D21210; BAA04751.1; -
EMBL; D21211; BAA04752.1; -
EMBL; X80289; CAA55563.1; -
EMBL; X79676; CAA56124.1; -
EMBL; L34583; AAC41755.1; -
EMBL; AF233323; AAF63474.1; -
EMBL; BC039610; AAH39610.1; ALT_TERM.
PIR; A54971; A54971.
PIR; I67629; I67629.
PIR; I67630; I67630.
PDB; 3PDZ; 17-MAR-00.
PDB; 1D5G; 24-JUL-02.
Genew; HGNC:9646; PTPN13.
MIM; 600267; -
GO; GO:0004725; P:protein tyrosine phosphatase activity; TAS.
GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
InterPro; IPR000299; Band 4.1.
InterPro; IPR001478; PDZ.
InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000242; TYR_PP.
Pfam; PF00373; Band 4.1; 1.
Pfam; PF00595; PDZ; 5.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR00935; BAND41.
PRINTS; PR00700; PRTYPHPTASE.
SMART; SM00295; B41; 1.
SMART; SM00228; PDZ; 5.
SMART; SM00194; PTPC; 1.
PROSITE; PS00660; FERM_1; FALSE NEG.
PROSITE; PS00661; FERM_2; FALSE NEG.
PROSITE; PS00507; FERM_3; 1.
PROSITE; PS0106; PDZ; 5.
PROSITE; PS00383; TYR PHOSPHATASE 1; FALSE_NEG.
PROSITE; PS00056; TYR PHOSPHATASE 2; 1.
PROSITE; PS00055; TYR PHOSPHATASE_PTP; 1.
KW Structural protein; Cytoskeleton; Hydrolase; Repeat; 3D-structu
KW Alternative splicing; Coiled coil; Polymorphism.
FT DOMAIN 56 59 POLY-LEU.
FT DOMAIN 572 872 FERM.
FT DOMAIN 2237 2485 PROTEIN-TYROSINE PHOSPHATASE.
FT DOMAIN 319 399 COILED COIL (POTENTIAL).
FT DOMAIN 469 504 COILED COIL (POTENTIAL).

Query Match 14.4%; Score 169; DB 1; Length 2485;
Best Local Similarity 28.4%; Pred. No. 0.0003;
Matches 40; Conservative 26; Mismatches 43; Indels 32;
QY 78 VNGCFEFAFATAKATVAFAASEGSHPR-----

RX MEDLINE=21143360; PubMed=11149944;
 RA Eichmüller S., Ueener D., Dummer R., Stein A., Thiel D.,
 RA Schandendorf D.;
 RT "Serological detection of cutaneous T-cell lymphoma-associated
 RT antigens.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:629-634 (2001).
 RN [17]
 RP SEQUENCE OF 857-1356 FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.J., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheet
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huly
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanci
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska A., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [8]
 RP INTERACTION WITH PARD6A.
 RX MEDLINE=20411249; PubMed=10954424;
 RA Johansson A.-S., Driesens M., Aspenstroem P.;
 RT "The mammalian homologue of the Caenorhabditis elegans polarity
 RT protein PAR-6 is a binding partner for the Rho GTPases Cdc42 at
 RT Rac1.";
 RL J. Cell Sci. 113:3267-3275 (2000).
 RN [9]
 RP SUBUNIT OF A COMPLEX CONTAINING PARD6B AND PRKCI.
 RC TISSUE=Kidney;
 RX MEDLINE=21157398; PubMed=11257119;
 RA Suzuki A., Yamana T., Hirose T., Manabe N., Mizuno K., Shimizu
 RA Akimoto K., Izumi Y., Ohnishi T., Ohno S.;
 RT "Atypical protein kinase C is involved in the evolutionarily con
 RT par protein complex and plays a critical role in establishing
 RT epithelia-specific junctional structures.";
 RL J. Cell Biol. 152:1183-1196 (2001).
 CC -1- FUNCTION: Adapter protein involved in asymmetrical cell divi
 CC and cell polarization processes. Seems to play a central ro
 CC the formation of epithelial tight junctions. Association w
 CC PARD6B may prevent the interaction of PARD3 with FHLR/JAM1,
 CC thereby preventing tight junction assembly. The PARD6-PARD3
 CC complex links GTP-bound Rho small GTPases to atypical prote
 CC Kinase C proteins.
 CC -1- SUBUNIT: Interacts with PARD6A and PARD6B. Isoform 2, but r
 CC least isoform 3 interacts with PRKCI. Interacts with PRKCI
 CC similarity). Part of a complex with PARD6A or PARD6B, PRKCI
 CC PRKCI and CDC42 or RAC1. Interacts with FHLR/JAM1 [By simi]
 CC SUBCELLULAR LOCATION: Cytoplasmic; membrane associated. Par
 CC localized along the cell-cell contact region. Colocalizes w
 CC PARD6A and PRKCI at epithelial tight junctions.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=10;
 CC Name=1; Synonyms=A;
 CC IsoId=Q8TEW0-1; Sequence=Displayed;
 CC Name=2; Synonyms=B, La;
 CC IsoId=Q8TEW0-2; Sequence=VSP_007464;
 CC Name=3; Synonyms=C;
 CC IsoId=Q8TEW0-3; Sequence=VSP_007465;
 CC Name=4; Synonyms=D;
 CC IsoId=Q8TEW0-4; Sequence=VSP_007466;
 CC

Qy	86	APATAKATVAAFAASGSHSRPV-----VELPKTDEGLGFNV-----MGKKE
Db	434	APASAPQNVFTTSSGYNKTKKRLKRLKQKKGTEGLGFSITSRDVTIG--
Qy	135	SRRIIPGVABRHGLKRGDQLLSVNGVSVEGHHKFAVELLKAAK--DSVKLVW
Db	491	KNILPRGNAQTODGLKAGDRLLIEVNGDVLGVKSQEVVSLRSTKKEGVLSLV

RESULT 14

ID	PAD3 MOUSE	PAD2 MOUSE	STANDARD	PRT	1333 AA
AC	Q99NEH2				
DT	10-OCT-2003 (Rel. 42, Created)				
DT	10-OCT-2003 (Rel. 42, Last sequence update)				
DE	Partitioning-defective 3 homolog (PARD-3) (PAR-3) (Atypical PKC isotype-specific interacting protein) (ASIP) (Ephrin interacting protein) (PHIP)				
DE	PARD3 OR PAR3				
OS	MUS musculus (Mouse)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M				
OC	NCBI_Taxid:10090				
RN	SEQUENCE FROM N.A. (ISOFORM 3).				
RP	STRAIN=NIH Swiss; TISSUE=Embryo;				
RC	MEDLINE=99121117; PubMed=9920925;				
RA	Lin D., Gish G.D., Songyang Z., Fawson T.;				
RT	"The carboxyl terminus of B class ephrins constitutes a PDZ dom				
RT	binding motif.";				
RL	J. Biol. Chem. 274:3726-3733(1999).				
RN	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3). SUBCELLULAR LOCATION,				
RP	PHOSPHORYLATION BY PRKCZ, INTERACTION WITH PRKCI AND PARD6A, SU				
RP	OF A COMPLEX CONTAINING PARD6A AND CDC42, AND MUTAGENESIS OF				
RP	824-SER--SER-826.				
RC	STRAIN=NIH Swiss;				
RC	MEDLINE=20394297; PubMed=10934475;				
RA	Lin D., Edwards A.S., Fawcett J.P., Mhamali G., Scott J.D., Paw				
RT	"A mammalian PAR-3-PAR-6 complex implicated in Cdc42/Rac1 and a				
RT	signalling and cell polarity.";				
RL	Nat. Cell Biol. 2:540-547(2000).				
RN	INTERACTION WITH PARD6B, AND SUBUNIT OF A COMPLEX CONTAINING PA				
RP	PRCI AND CDC42.				
RP	MEDLINE=20394296; PubMed=10934474;				
RA	Joberty G., Petersen C., Gao L., Macara I.G.;				
RT	"The cell-polarity protein Par6 links Par3 and atypical protein				
RT	C to Cdc42.";				
RL	Nat. Cell Biol. 2:531-539(2000).				
RN	INTERACTION WITH F1LR.				
RP	MEDLINE=21340266; PubMed=11447115;				
RA	Ebnet K., Suzuki A., Horikoshi Y., Hirose T.,				
RA	Meyer zu Bruckwedde M.-K., Ohno S., Vestweber D.;				
RT	"The cell polarity protein ASIP/PA3-3 directly associates with				
RT	junctional adhesion molecule (JAM).";				
RL	EMBO J. 20:3738-3748(2001).				
RN	INTERACTION WITH F1LR AND PARD6B.				
RP	MEDLINE=21828709; PubMed=11839275;				
RA	Gao L., Joberty G., Macara I.G.;				
RT	"Assembly of epithelial tight junctions is negatively regulated				
RT	Par6.";				
RL	Curr. Biol. 12:221-225(2002).				

-!- FUNCTION: Adapter protein involved in asymmetrical cell divi and cell polarization processes. Plays a role in the format epithelial tight junctions. Association with PARD6B may pre the interaction of PAR3 with F1LR/JAM1, thereby preventing junction assembly. The PARD6-PARD3 complex links GTP-bound small GTPases to atypical protein kinase C proteins.

-!- SUBUNIT: Interacts with PARD6A, PARD6B, PRKCI and PRKCZ. Pa

519 LAKSQBQEWLSLIRSTXMEGTVSLIVFRQBEAFHPR---EMNAEPSSQMQTPKEI

RESULT 15

ID	PAD3	RAT	STANDARD;	PRT;	1337 AA.
AC	Q92340;				
AC	10-OCT-2003 (Rel. 42, Created)				
DT	10-OCT-2003 (Rel. 42, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Partitioning-defective 3 homolog (PARD-3) (PAR-3) (Atypical PKC isotype-specific interacting protein) (ASIP) (Atypical PKC specific binding protein) (ASBP).				
DE	PARD3 OR PAR3.				
GN	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; R				
OC	NCBI_TaxId:10116;				
RP	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH PRKCI AND				
RP	TISSUE=Fibroblast;				
RC	MEDLINE=98437350; PubMed=9763423;				
RC	Izumi Y., Hirose T., Tamai Y., Hirai S.-I., Nagashima Y., Fujim				
RA	Takabe Y., Kempkes K.J., Ohno S.;				
RA	"An atypical PKC directly associates and colocalizes at the epi				
RT	tight junction with ASIP, a mammalian homologue of caenorhabdit				
RT	elegans polarity protein PAR-3. "				
RT	J. Cell Biol. 143:95-106(1998).				
RL	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM 2), SUBCELLULAR LOCATION, AND				
RP	PHOSPHORYLATION OF SER-827.				
RP	MEDLINE=22040490; PubMed=12045219;				
RC	Hirose T., Izumi Y., Nagashima Y., Tamai-Nagai Y., Kurihara H.,				
RA	Sakai T., Suzuki Y., Yamanaka T., Suzuki A., Mizuno K., Ohno S.				
RA	"Involvement of ASIP/PAR-3 in the promotion of epithelial tight				
RT	junction formation. "				
RT	J. Cell Sci. 115:2485-2495(2002).				
RL	[-] FUNCTION: Adapter protein involved in asymmetrical cell divi				
CC	and cell polarization processes. Seems to play a central ro				
CC	the formation of epithelial tight junctions. Association wi				
CC	PARD6B may prevent the interaction of PARD3 with FHLR/JAM1,				
CC	thereby preventing tight junction assembly. The PARD6-PARD3				
CC	complex links GTP-bound Rho small GTPases to atypical prote				
CC	kinase C proteins.				
CC	[-] SUBUNIT: Interacts with PARD6A, PARD6B and FHLR/JAM1 via it				
CC	domain (By similarity). Interacts with PRKCI. Interacts wit				
CC	(probable). Part of a complex with PARD6A or PARD6B, PRKCI				
CC	PRKCB and CDC42 or RAC1 (By similarity).				
CC	[-] SUBCELLULAR LOCATION: Cytoplasmic; membrane associated. Loc				
CC	along the cell-cell contact region. Colocalizes with PRKCB				
CC	apical edge of tight junctions.				
CC	[-] ALTERNATIVE PRODUCTS:				
CC	Event=Alternative splicing; Named isoforms=2;				
CC	Name=1; Synonyms=180 kDa;				
CC	Isoid=092340-1; Sequence=Displayed;				
CC	Name=2; Synonyms=150 kDa;				
CC	Isoid=092340-2; Sequence=VSP_007475;				
CC	[-] TISSUE SPECIFICITY: Isoform 1 is predominantly expressed in				
CC	glandular stomach, prostate, ovary and uterus. Isoform 1 is				
CC	expressed in brain, with a high expression in the cortex,				
CC	hippocampus and in the striatum. Isoform 2 is predominantly				
CC	expressed in intestinal epithelial cells, kidney and prosta				
CC	[-] PTM: Phosphorylated by PRKCB (By similarity). The phosphory				
CC	form is concentrated at the most apical tip of cell-cell co				
CC	during the initial phase of tight junction formation.				
CC	[-] SIMILARITY: Belongs to the PAR3 family.				
CC	[-] SIMILARITY: Contains 3 PDZ/DHR domains.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a co				
CC	between the Swiss Institute of Bioinformatics and the EMBL o				
CC	the European Bioinformatics Institute. There are no restricti				
CC	use by non-profit institutions as long as its content is				
CC	modified and this statement is not removed. Usage by and for				

549; BAA34216.1; -.

3; 3PDZ.

95; PDZ; 3.

50106; PDZ;

; phosphorylation

461 546

712 550
984 1042

1149 1172

1278 1299

1034 1337

L33 / AA; I494.

ilarity 37.0%

1
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12

REGISTRATION

PKVL EEMFARFEKT.E

PR-- --EMNAEPSQMQ

57

GenCore version 5.1.1.6
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tein search, using sw model

March 18, 2004, 13:22:34 ; Search time 45 Seconds
(without alignments)
1633.683 Million cell updates/sec

US-09-909-005-1

1170
1 MEKPSVTSAPTADMATLVV.....LLIQQQQQQQQQTQQNHMS 233

BLOSUM62

Gapop 10.0 , Gapext 0.5

1017041 segs, 315518202 residues

hits satisfying chosen parameters: 1017041

length: 0

length: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

SPTREMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvrius.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	DB	ID	Description
100.0	233	4	014910		014910 homo sapien
92.1	219	11	Q92250		Q92250 rattus norv
90.3	211	11	Q8JZS0		Q8JZS0 mus musculu
69.6	197	4	Q9NUP9		Q9NUP9 homo sapien
69.6	197	11	Q88952		Q88952 mus musculu
69.4	197	13	Q7ZVU3		Q7ZVU3 xenopus lae
69.1	207	11	Q88951		Q88951 mus musculu
69.1	207	11	Q92252		Q92252 rattus norv
69.0	207	4	Q9HAP6		Q9HAP6 homo sapien
64.8	182	11	Q92251		Q92251 rattus norv
64.4	195	5	Q9VBY7		Q9VBY7 drosophila
58.5	244	5	Q8IMT8		Q8IMT8 schistosoma
55.4	171	5	Q17458		Q17458 schistosoma
55.3	316	5	Q9U245		Q9U245 caenorhabdi
55.0	297	5	P90976		P90976 caenorhabdi
20.0	967	5	Q9BI79		Q9BI79 caenorhabdi

17	233.5	20.0	1064	5	Q18165	Q18165 ca
18	220	18.8	946	5	Q7YXH8	Q7YXH8 dr
19	219	18.7	852	11	Q91XM9	Q91XM9 pi
20	208.5	17.8	960	5	Q9VYZ4	Q9VYZ4 dr
21	208.5	17.8	968	5	Q9VYZ5	Q9VYZ5 dr
22	203.5	17.4	950	11	Q80TH1	Q80TH1 pi
23	199.5	17.1	403	11	Q8BSV4	Q8BSV4 pi
24	199.5	17.1	455	11	Q9ET11	Q9ET11 pi
25	199.5	17.1	455	11	Q920R1	Q920R1 pi
26	199.5	17.1	463	11	Q8BH60	Q8BH60 pi
27	198.5	17.0	454	4	Q969U8	Q969U8 hc
28	198.5	17.0	462	4	Q9HD26	Q9HD26 hc
29	196.5	16.8	721	11	Q91WJ1	Q91WJ1 pi
30	192	16.4	893	11	Q8CGN7	Q8CGN7 pi
31	192	16.4	905	11	Q81ID0	Q81ID0 pi
32	191.5	16.4	2055	11	Q921K3	Q921K3 pi
33	190.5	16.3	873	13	Q7ZUM2	Q7ZUM2 l
34	188.5	16.1	164	11	Q8C0H8	Q8C0H8 pi
35	187.5	16.0	526	11	Q08783	Q08783 pi
36	187.5	16.0	1124	11	Q80ZY8	Q80ZY8 m
37	187.5	16.0	2055	11	Q8VBY0	Q8VBY0 m
38	187.5	16.0	2055	11	Q8VRV5	Q8VRV5 m
39	187.5	16.0	2055	11	Q8VEX6	Q8VEX6 m
40	186.5	15.9	2054	11	Q55164	Q55164 i
41	186	15.9	920	13	Q90X35	Q90X35 b
42	185	15.8	927	11	Q62402	Q62402 m
43	178.5	15.3	519	11	Q80TZ1	Q80TZ1 m
44	178.5	15.3	526	11	Q8K4T6	Q8K4T6 x
45	178.5	15.3	532	11	Q7TQL6	Q7TQL6 m

ALIGNMENTS

RESULT 1

014910	PRELIMINARY;	PRT;	233 AA.
ID	014910		
AC	014910;		
DT	01-MAY-1998 (TRENBLrel. 05, Created)		
DT	01-MAY-1999 (TRENBLrel. 10, Last sequence update)		
DT	01-OCT-2003 (TRENBLrel. 25, Last annotation update)		
DE	VELI 1 (YAX interaction protein 33) (Fragment).		
GN	MALS-1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Testis;		
RX	MEDLINE=98424246; PubMed=9753324;		
RA	Butz S., Okamoto M., Sudhof T.C.;		
RT	"A tripartite protein complex with the potential to couple syna		
RT	vesicle exocytosis to cell adhesion in brain.";		
RL	Cell 94:773-782(1998).		
RN	[2]		
RP	SEQUENCE OF 32-233 FROM N.A.		
RA	Rousset R., Fabre S., Desbois C., Bantignies F., Jalinot P.;		
RL	Oncogene 15:0-0(1997).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99274724; PubMed=10341223;		
RA	Jo K., Derin R., Li M., Bredt D.S.;		
RT	"Characterization of MALS/Velis-1, -2, and -3: a family of mamm		
RT	LIN-7 homologs enriched at brain synapses in association with t		
RT	postsynaptic density-95/NMDA receptor postsynaptic complex.";		
RL	J. Neurosci. 19:4189-4199(1999).		
CC	-1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.		
DR	EMBL; AF087693; AAC78481.1;		
DR	EMBL; AF028826; AAB84251.1;		
DR	EMBL; AF173081; AAD48500.1;		
DR	HSP; Q12923; 3PDZ.		
DR	Genew; HGNC:17787; LIN7A.		

```

15; F:protein binding; IPI.
87; P:exocytosis; TAS.
61; P:protein complex assembly; TAS.
R004172; L27.
8; L27; 1.
5; PDZ; 1.
69; L27; 1.
28; PDZ; 1.
0106; PDZ; 1.
1
33 AA; 25997 MW; D8D05EF16A93BE7B CRC64;
    100.0%; Score 1170; DB 4; Length 233;
    Identity 100.0%; Pred. No. 2.2e-86;
    Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PSTSAPTADMATLVVQPLTLDROVARAIELEKLEQESGEVPHKLSLKVQSE 60
PSTSAPTADMATLVVQPLTLDROVARAIELEKLEQESGEVPHKLSLKVQSE 60
AIREVQVYMHETIIVNGCPEFRARATATVAFAASEGHSHPRVWELPKTDEGLGF 120
AIREVQVYMHETIIVNGCPEFRARATATVAFAASEGHSHPRVWELPKTDEGLGF 120
GGKQNSPIYISRIIPGVVAERHGLKRGDQLLSVNGSVSVEGEHEKAVELLKAAKD 180
GGKQNSPIYISRIIPGVVAERHGLKRGDQLLSVNGSVSVEGEHEKAVELLKAAKD 180
LVRYTPKVLSEMEAREFEKLTARRRQQQLLIQQOQQOQQOQQOQQOQHMS 233
LVRYTPKVLSEMEAREFEKLTARRRQQQLLIQQOQQOQQOQQOQQOQHMS 233

PRELIMINARY; PRT; 219 AA.
(TEMBLrel. 10, Created)
(TEMBLrel. 10, Last sequence update)
(TEMBLrel. 24, Last annotation update)
gicus (Rat).
teazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
0116;
M N.A.
9097; PubMed=10362251;
a Y., Deguchi M., Ide N., Hirao K., Yao I., Nishioka H.,
and characterization of mammalian homologues of
is elegans lin-7: localization at cell-cell junctions.;
2811-2817(1999).
TY; CONTAINS 1 PDZ/DHR DOMAIN.
35; AAC78074.1; -.
; 3PDZ.
42; P:intracellular signaling cascade; IEA.
R004172; L27.
R001478; PDZ.
8; L27; 1.
5; PDZ; 1.
69; L27; 1.
28; PDZ; 1.
0106; PDZ; 1.
19 AA; 24549 MW; 6EB6A4AFC5C1EC74 CRC64;
    92.1%; Score 1077.5; DB 11; Length 219;
    Identity 98.6%; Pred. No. 5.7e-79;
    Conservative 0; Mismatches 2; Indels 1; Gaps 1;

LTVVQPLTLDROVARAIELEKLEQESGEVPHKLSLKVQSEFCTAIREVQVYMH 73
|||||

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Db 1 MATLVVQPLTLDROVARAIELEKLEQESGEVPHKLSLKVQSEFCTAIREV
Qy 74 ETTVNGCPEFRARATATVAFAASEGHSHPRVWELPKTDEGLGFNVGKGC
Db 61 ETTVNGCPEFRARATATVAFAASEGHSHPRVWELPKTDEGLGFNVGKGC
Qy 134 ISRIIPGVVAERHGLKRGDQLLSVNGSVSVEGEHEKAVELLKAAKDSVKLVVRY
Db 121 ISRIIPGVVAERHGLKRGDQLLSVNGSVSVEGEHEKAVELLKAAKDSVKLVVRY
Qy 194 EMEAREFEKLTARRRQQQLLIQQOQQOQQOQQOQQOQHMS 233
Db 181 EMEAREFEKLTARRRQQQLLIQQOQQOQQOQQOQQOQHMS 219

RESULT 3
Q8JZS0 PRELIMINARY; PRT; 211 AA.
AC Q8JZS0;
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Similar to vertebrate LIN7 homolog 1, Tax interaction protein 33
DE (Fragment).
GN LIN7A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
DR EMBL; BC029721; AAH29721.1; -.
DR MGD; MGI:2135609; Lin7a.
DR GO; GO:0016323; C:basolateral plasma membrane; IDA.
DR InterPro; IPR004172; L27.
DR InterPro; IPR001478; PDZ.
DR Pfam; PF02828; L27; 1.
DR Pfam; PF00595; PDZ; 1.
DR SMART; SM00569; L27; 1.
DR SMART; SM00228; PDZ; 1.
DR PROSITE; PS0106; PDZ; 1.
FT NON TER 1
SQ SEQUENCE 211 AA; 23752 MW; 73ADE354FC8BEE83 CRC64;

Query Match 90.3%; Score 1057; DB 11; Length 211;
Best Local Similarity 99.5%; Pred. No. 2.4e-77;
Matches 210; Conservative 0; Mismatches 1; Indels 0;

Qy 23 LTLDROVARAIELEKLEQESGEVPHKLSLKVQSEFCTAIREVQVYMHETI
Db 1 LTLDROVARAIELEKLEQESGEVPHKLSLKVQSEFCTAIREVQVYMHETI
Qy 83 EFRARATATVAFAASEGHSHPRVWELPKTDEGLGFNVGKGEQNSPIYISR
Db 61 EFRARATATVAFAASEGHSHPRVWELPKTDEGLGFNVGKGEQNSPIYISR
Qy 143 AERHGLKRGDQLLSVNGSVSVEGEHEKAVELLKAAKDSVKLVVRYTPKVLSEME
Db 121 AERHGLKRGDQLLSVNGSVSVEGEHEKAVELLKAAKDSVKLVVRYTPKVLSEME
Qy 203 LRTARRRQQQLLIQQOQQOQQOQQOQQOQHMS 233
Db 181 LRTARRRQQQLLIQQOQQOQQOQQOQQOQHMS 211

RESULT 4
Q9NUP9 PRELIMINARY; PRT; 197 AA.
AC Q9NUP9;

```

[illegible]

99097; PubMed=10362251;
 Yama Y., Deguchi M., Ide N., Hirao K., Yao I., Nishioka H.,
 and characterization of mammalian homologs of
 the *Xenopus laevis* elegans lin-7: localization at cell-cell junctions.";
 12811-2817 (1999).
 ITY: CONTAINS 1 PDZ/DHR DOMAIN.
 133; AAC78072.1; -.
 3; 3PDZ.
 142; P:intracellular signaling cascade; IEA.


```

AL--VEPGLGEROVSRAVELLERLQSGELPPQKQLQORVLQSRFCSAIREVYSQLY 50
ITWNGCPFRARATAKATVAAPAASEGSHSPRVVELPKTDEGLGNVMGKGQNPIY 133
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
LDITGSASIRAHATAKATVAAPTASEGHAHPRVVELPKTDEGLGNVMGKGQNPIY 118
RIIPGVVAERHGGLKRGDQLLSVNGSVSEGEHEKAVALLEAAKDSVKLVRYTPKVL 193
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RVIIPGVVADRHHGLKRGDQLLSVNGSVSEGEHEKAVALLEAAKDSVKLVRYTPKVL 178
MEARFEKLRTARRRQQOQ 213
MEARFEKWRSARRRQQHQ 198
PRELIMINARY; PRT; 162 AA.
(TREMBLrel. 10, Created)
(TREMBLrel. 10, Last sequence update)
(TREMBLrel. 24, Last annotation update)
sgicus (Rat).
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Ichtheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
10116;
OM N.A.
39097; PubMed=10362251;
Sa Y., Deguchi M., Ide N., Hirao K., Yao I., Nishioka H.,
and characterization of mammalian homologues of
this elegans lin-7: localization at cell-cell junctions.";
2811-3817(1999)
TRY: CONTAINS 1 PDZ/DHR DOMAIN.
134; AAC78073.1; -.
}; 3PDZ.
242; P;intracellular signaling cascade; IEA.
PR004172; L27.
PR001478; PDZ.
28; L27; 1.
35; PDZ; 1.
369; L27; 1.
228; PDZ; 1.
50106; PDZ; 1.
182 AA; 19927 MW; D448E3BBCFSA51DB CRC64;
64.8%; Score 758; DB 11; Length 182;
ilarity 98.7%; Pred.No.2.5e-53;
Conservative 2; Mismatches 0; Indels 0; Gaps 0
TLTVVPQTLDROVARAIELLEKLQESGPVPHKLSKKVLQSEFTCTAREVQYMH 73
TLTVVPQLTDROVARAIELLEKLQESGPVPHKLSKKVLQSEFTCTAREVQYMH 60
ITWNGCPFRARATAKATVAAPAASEGSHSPRVVELPKTDEGLGNVMGKGQNPIY 133
ITWNGCPFRARATAKATVAAPAASEGSHSPRVVELPKTDEGLGNVMGKGQNPIY 120
RIIPGVVAERHGGLKRGDQLLSVNGSVSE 164
RIIPGVVAERHGGLKRGDQLLSVNGVALE 151
PRELIMINARY; PRT; 195 AA.
(TREMBLrel. 13, Created)
(TREMBLrel. 13, Last sequence update)
(TREMBLrel. 24, Last annotation update)
ain.

```

CORINTHIOS 195

THE UNIVERSITY OF CHICAGO

DR	InterPro; IPR004172; L27.
DR	InterPro; IPR001478; PDZ.
DR	Pfam; PF02828; L27; 1.
DR	Pfam; PF00595; PDZ; 1.
DR	SMART; SM00569; L27; 1.
DR	SMART; SM00228; PDZ; 1.
DR	PROSITE; PS50106; PDZ; 1.
SQ	SEQUENCE 316 AA; 35663 MW; E050959F2D29BFF CRC64;
Query Match 55.3%; Score 647.5; DB 5; Length 316;	
Best Local Similarity 67.9%; Pred.No. 4.1e-44;	
Matches 129; Conservative 30; Mismatches 30; Indels 1;	
QY	25 LRDVVAIAELLEKLOESGEVPVHKLSIKKVLOSSECTAIRREVQYMHEITIV
DB	117 LERDVQRILMEHVQKTGCVNNAKLASLQQVLQSEFFGAHVETVYESIDAI
QY	85 RARATKATVAFAASEGHSPRVVELPKTDEGLGFNMVGKEQNSPIYSRIIH
DB	177 KAATAKATVAFAAAGHAPRIVELPKTDQGLGFNMVGKEQNSPIYSRIIH
QY	145 RHGGIKRGDDLSVNGSVSGEHEHKAVALLKAAKOVSUKLVIRYTPKVLDEMAI
DB	237 RHGGIKRGDDLTAVNG-NVEAECHKAVDLLKSASGVGSVKIVRYMPKLIDEMERI
QY	205 TARRRRQQQL 214
DB	296 IRSTQQSPTL 305
RESULT 15	
P90976	PRELIMINARY; PRT; 297 AA.
ID	P90976 AC
DT	01-MAY-1997 (TrEMBLrel. 03, Created)
DT	01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DE	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE	LIN-7 (Fragment)
OS	Caenorhabditis elegans.
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoi
OX	Rhabditidae; Peloderinae; Caenorhabditis.
CX	NCBI_Taxid=6239;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE-96200771; PubMed-8612272;
RA	Simske J.S., Kaech S.M., Harp S.A., Kim S.K.;
RT	"LET-23 receptor localization by the cell junction protein LIN-7
RT	during C. elegans vulval induction.";
CC	Cell 85:195-204(1996).
CC	-1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
DR	EWBL; U78092; AAB36684.1; -;
DR	HSSP; Q12959; IPDR.
DR	GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR	InterPro; IPR004172; L27.
DR	InterPro; IPR001478; PDZ.
DR	Pfam; PF02828; L27; 1.
DR	Pfam; PF00595; PDZ; 1.
DR	SMART; SM00569; L27; 1.
DR	SMART; SM00228; PDZ; 1.
DR	PROSITE; PS50106; PDZ; 1.
FT	NON TER 297
SQ	SEQUENCE 297 AA; 33580 MW; A8F15EDB90BA0E CRC64;
Query Match 55.0%; Score 643.5; DB 5; Length 297;	
Best Local Similarity 70.6%; Pred.No. 7.9e-44;	
Matches 127; Conservative 29; Mismatches 23; Indels 1;	
QY	25 LRDVVAIAELLEKLOESGEVPVHKLSIKKVLOSSECTAIRREVQYMHEITIV
DB	117 LERDVQRILMEHVQKTGCVNNAKLASLQQVLQSEFFGAHVETVYESIDAI
QY	85 RARATKATVAFAASEGHSPRVVELPKTDEGLGFNMVGKEQNSPIYSRIIH

15:31:26 2004

us-09-909-005-1.rpt

AATAKATVAFAAAEGHAHPRIVELPKTDQGLGFMGKGQNSPIYISRIIPGGVAD 236

GGLKRGDOLLSVNGSVGEHEHKAVELLKAADSVKLVVRYTPKVLLEMEARFEKLR 204

SGLKRGDOLIAVNG-NVEAECHERKAVDLKSAVGSVKLVIRYMPKLLDENERRFERQR 295

: March 18, 2004, 13:28:20
CS

15:31:25 2004

us-09-909-005-1.rag

GenCore version 5.1.6
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tein search, using sw model

March 18, 2004, 13:19:49 ; Search time 59 Seconds
(without alignments)
1115.823 Million cell updates/sec

US-09-909-005-1

1170
1 MLKPSVTSAPTADMATLVV.....ILLIQQQQQQQQQTQNHMS 233

BLOSUM62

Gapop 10.0 , Gapext 0.5

1586107 seqs, 282547505 residues

hits satisfying chosen parameters: 1586107

length: 0
ength: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

A_Geneseq 23Jan04: *
1: Geneseq1980s: *
2: Geneseq1990s: *
3: Geneseq2000s: *
4: Geneseq2001s: *
5: Geneseq2002s: *
6: Geneseq2003as: *
7: Geneseq2003bs: *
8: Geneseq2004s: *

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

Query Match	Length	DB	ID	Description
100.0	233	2	AA29978	Aay29978 Human cel
100.0	233	4	AAU07127	Aau07127 Human cel
100.0	233	5	AAU99326	Aau99326 Human cel
100.0	233	7	ADD46702	Add46702 Human Pro
100.0	233	7	AD55392	Ad55392 Human Pro
89.6	197	4	AAW78892	Aaw78892 Human pro
89.6	197	4	AA93600	Aab93600 Human pro
89.6	198	4	AAW9876	Aam79876 Human pro
69.0	207	4	AAE03655	Aae03655 Human ext
69.0	207	5	AAU83629	Aau83629 Human PRO
69.0	207	6	ABU80776	Abu80776 Human PRO
69.0	207	6	ABO33742	Abc33742 Novel hum
69.0	207	6	ABU82085	Abu82085 Novel hum
69.0	207	6	ABJ72265	Abj72265 Human PRO
69.0	207	6	ABJ72393	Abj72393 Human PRO
69.0	207	6	ABO34288	Abc34288 Human sec
69.0	207	7	ABJ72095	Abj72095 Human mem
69.0	207	7	ADB83566	Adb83566 Novel hum
69.0	207	7	ABU80672	Abu80672 Novel hum
69.0	207	7	ABD73213	Abd73213 Novel hum
69.0	207	7	ABD78295	Abd78295 Novel hum
69.0	207	7	ADB84943	Adb84943 Human PRO
69.0	207	7	ABD78049	Adb78049 Novel hum
69.0	207	7	ABD87115	Adb87115 Human PRO
69.0	207	7	ADB84697	Adb84697 Human PRO

26	807	69.0	207	7	ADB83812	Adb83812
27	807	69.0	207	7	ADB72967	Adb72967
28	807	69.0	207	7	ADC36805	Adc36805
29	807	69.0	207	7	ADC21795	Adc21795
30	807	69.0	207	7	ADC49826	Adc49826
31	807	69.0	207	7	ADC49025	Adc49025
32	807	69.0	207	7	ADC49542	Adc49542
33	807	69.0	207	7	ADC47403	Adc47403
34	807	69.0	207	7	ADC47148	Adc47148
35	807	69.0	207	7	ADC78023	Adc78023
36	807	69.0	207	7	ADD06258	Add06258
37	807	69.0	207	7	ADC77777	Adc77777
38	807	69.0	207	7	ADD50740	Add50740
39	807	69.0	207	7	ADD50986	Add50986
40	807	69.0	207	7	ADD50467	Add50467
41	807	69.0	207	7	ADD50221	Add50221
42	807	69.0	207	7	ADD51232	Add51232
43	807	69.0	207	8	ADC48779	Adc48779
44	807	69.0	207	8	ADE20950	Ade20950
45	807	69.0	207	8	AD05794	Ad05794

ALIGNMENTS

RESULT 1
AA29978
ID AAY29978 standard; protein; 233 AA.
XX
AC AAY29978;
XX
DT 23-NOV-1999 (first entry)
XX
DE Human cell junction PDZ protein CUPDZ.
XX
KW Human; cell junction PDZ protein; PDZ domain; CUPDZ; diagnosis;
KW neurological disorder; developmental disorder; William's syndr
XX
OS Homo sapiens.
XX
PN US5958731-A.
XX
PD 28-SEP-1999.
XX
PF 11-SEP-1998; 98US-00151611.
XX
PR 11-SEP-1998; 98US-00151611.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Yue H, Patterson C, Au-Young J;
XX
DR WPI; 1999-561035/47.
DR N-PSDB; AA221259.
XX
PT Nucleic acids encoding cellular junction PDZ protein domains us
PT the prevention, diagnosis and treatment of disorders associated
PT defective cell signaling such as cancers and neurological and
PT developmental disorders.
XX
PS Claim 1; Col 39-40; 27pp; English.
XX
CC The present sequence represents human cell junction PDZ protein
CC CUPDZ polynucleotides and proteins may be used in the diagnosis
CC prevention and treatment of disorders associated with defective
CC signalling. They may be used to treat cancers, neurological dis
CC developmental disorders such as William's syndrome. CUPDZ or ve
CC containing CUPDZ may be administered to treat any of the above
CC by rectifying mutations or deletions in a patient's genome that
CC cell signalling by expressing inactive proteins or to supplemen
CC patients own production of CUPDZ protein domains. Antisense nuc
CC molecules may be administered to down regulate CUPDZ protein dc
CC expression by binding with the cells own CUPDZ genes and preven

CJPDZ polynucleotides may also be used as DNA probes in assays to detect and quantitate the presence of similar sequences in samples, and hence which patients may be in need of therapy. They may also be used to study the structure and function of CJPDZ protein domains and their role in signalling. The CJPDZ protein domains may be used as antigens in the production of antibodies and in assays to identify modulators of signalling and activity.

```

AA;
        100.0%; Score 1170; DB 2; Length 233;
        Identity 100.0%; Pred. No. 7.5e-108;
        Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CPSTVTSAPTADMATVTVQPLTLDVRAIAELLEKLOESGEVPHKLSLQSE 60
|||||
CPSTVTSAPTADMATVTVQPLTLDVRAIAELLEKLOESGEVPHKLSLQSE 60

FAIREVYQVMHETITVNGCPEFRARATATVAFAASEGSHSPRVVLPKTDGLGF 120
|||||
FAIREVYQVMHETITVNGCPEFRARATATVAFAASEGSHSPRVVLPKTDGLGF 120

KGKQEQNSPIYISRIIPGVAERHGGIKRGDQLLSVNGSVSEGEHHEKAVELLKAAKD 180
|||||
KGKQEQNSPIYISRIIPGVAERHGGIKRGDQLLSVNGSVSEGEHHEKAVELLKAAKD 180

CLVRYTPKVLSEMEAREPEKLTARRRQQQLLIQ00000000000000000000HMS 233
|||||
CLVRYTPKVLSEMEAREPEKLTARRRQQQLLIQ00000000000000000000HMS 233

```

Standard; protein; 233 AA.

(first entry)

unction PDZ protein, CJPDZ.

unction PDZ protein; CJPDZ; antigen; antibody; cytostatic; anti-neuroprotective; anti-epileptic; anti-Alzheimer's disease; anti-convulsant; cancer; leukaemia; myeloma; sarcoma; disorder; epilepsy; Alzheimer's disease; chorea.

Location/Qualifiers
107..189
/label= PDZ_domain

98US-00370102.

98US-00151611.

TE GENOMICS INC.

Young J, Patterson C;

3943/50.
1583.

action PDZ proteins useful in the prevention, diagnosis and disorders associated with defective cell signalling such as neurological disorders and developmental disorders such as syndrome.

XX Claim 1; Fig 1; 28pp; English.
PS The invention relates to a purified human cell junction PDZ (CJPDZ) polypeptide. The polypeptide may be used as an antigen in the production of antibodies against CJPDZ and in assays to identify molecules that bind CJPDZ including modulators of CJPDZ expression and activity.
CC anti-CJPDZ antibodies, agonists and antagonists may be used to control/regulate expression and activity of CJPDZ. The anti-CJPDZ antibodies may also be used as diagnostic agents for detecting the presence of CJPDZ polypeptides in samples (e.g. by enzyme linked immunosorbent assay, ELISA). Disorders of cell signalling and expression and activity that may be prevented, diagnosed and/or treated by the above methods include, for example cancers (e.g. leukaemia, myeloma, sarcoma or lung, liver, colon or spleen cancer), neurological disorders (e.g. epilepsy, Alzheimer's disease and/or Huntington's chorea). A full list of disorders that may be treated is given in the specification. The present sequence represents human CJPDZ.

XX Sequence 233 AA;

Query Match 100.0%; Score 1170; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 7.5e-108;
Matches 233; Conservative 0; Mismatches 0; Indels 0;

```

Qy 1 MKPSVTSAPTADMATVTVQPLTLDVRAIAELLEKLOESGEVPHKLSLQSE 1
Db 1 MKPSVTSAPTADMATVTVQPLTLDVRAIAELLEKLOESGEVPHKLSLQSE 1
Qy 61 FCTAIREVYQVMHETITVNGCPEFRARATATVAFAASEGSHSPRVVLPKTI 61
Db 61 FCTAIREVYQVMHETITVNGCPEFRARATATVAFAASEGSHSPRVVLPKTI 61
Qy 121 NVMGKEQNSPIYISRIIPGVAERHGGIKRGDQLLSVNGSVSEGEHHEKAVELI 121
Db 121 NVMGKEQNSPIYISRIIPGVAERHGGIKRGDQLLSVNGSVSEGEHHEKAVELI 121
Qy 181 SVKLVRVYTPKVLSEMEAREPEKLTARRRQQQLLIQ0000000000000000HMS 181
Db 181 SVKLVRVYTPKVLSEMEAREPEKLTARRRQQQLLIQ0000000000000000HMS 181

```

RESULT 3

AAU99326

ID AAU99326 standard; protein; 233 AA.

XX AAU99326;

DT 07-OCT-2002 (first entry)

DE Human cell junction PDZ (CJPDZ) protein.

KW Human; cytostatic; neurotropic; neuroprotective; endocrine; cell junction PDZ; CJPDZ; membrane-associated signalling protein signal transduction; postsynaptic density protein 95; PSD-95; Drosophila lethal (1) discs large-1; Dlg; zonula occludens-1; ZC cell signalling; cancer; leukaemia; lymphoma; neurological disorder; Alzheimer's disease; Parkinson's disease; developmental disorder; muscular dystrophy; William's syndrome.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Domain 107..189

FT /note= "Putative PDZ domain"

XX US2002082388-A1.

XX 27-JUN-2002.

XX 18-JUL-2001; 2001US-00909005.

XX 11-SEP-1998; 98US-00151611.

99US-00370102;

TE PHARM INC.

Young J, Patterson C;

37135/57.

37047.

function PDZ protein domains useful in the prevention, diagnosis and treatment of disorders associated with defective cell signaling such as neurological disorders and developmental disorders such as autism.

p 1: 31pp: English.

son discloses a human cell junction PDZ (CUPDZ) polypeptide and a nucleotide encoding it. PDZ is a conserved protein domain which is present in various membrane-associated signalling proteins. These proteins play a key role in the regulation and coordination of intracellular signalling pathways. PDZ domains were first identified in -

1. density protein 95 (DP-95), Drosophila lethal (1) discs large (Dlg) and zonula occludens-1 (ZO-1). The polypeptides and nucleotide sequences of these proteins can be used to diagnose or treat a disease or condition associated with decreased expression of functional CUPDZ, for screening for effectiveness as agonists or antagonists, for screening for compounds that modulates the protein activity, for screening compounds for altering gene expression and for raising antibodies. PDZ domains and polynucleotides are useful for the prevention, diagnosis and treatment of disorders associated with defective cell junction proteins such as cancers (e.g. leukaemia and lymphoma), neurological disorders (e.g. Alzheimer's disease and Parkinson's disease) and other disorders (e.g. muscular dystrophy and Williams syndrome). The present invention is the human cell junction PDZ (CUPDZ) protein.

AA:

100.0%: Score 1170: DB 5: Length 233:

Similarity 100.0%; pred. No. 7.5e-108;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CPSVTSAPTADMATLTVVQPLTLDRDVARAIELLEKLEQESGEVPVHKLSLKKVLQSE 60

CPSVTSAPTADMATLTVVQPLTLDRDVARAIELLEKQESGEVPVHKLSLKKVLQSE 60

PAIREVYQYMHETITVNGCPEFRARATAKATVAFAASEGHSHPRVVELPKTDEGLGF 120

TAIREVYOYMHETITVNGCPEFRARATAKATVAFAASEGHSHPRVVELPKTDEGLGF 120

GGGKEONSPIYTSRITPGGVAERHGGIKRGDOLI.SVNGVSVGEHEHEKAVEI.I.KAAKD 180

MGCKEONSPITYSRITPGGVAERHGGIKRGDOIISVNGVSVEGEHHEKAVETIKAAKD180

KI WVRYTPKVI REMEAP EEKI RTARRP00000I.I.000000000000T00CNHMS 233

ИД ИВУТЮЛ ЗЕМЕАРБЕКІ БТАРБВОАССЫ І ТАООООООООООООООООО

andard; protein; 233 AA.

(first entry)

in NP 004655, SEO ID NO 12387.

; neuronal tissue; gene therapy;
 ental nerve injury; chronic constriction injury; CCI;
 e injury; SNI; Chung.

XX	Homo sapiens.
OS	
XX	WC2003016475-A2.
XX	
XX	27-FEB-2003.
PD	
XX	14-AUG-2002; 2002WO-US025765.
XX	
XX	14-AUG-2001; 2001US-0312147P.
PR	
PR	01-NOV-2001; 2001US-0346382P.
PR	
PR	26-NOV-2001; 2001US-0333347P.
XX	
PA	(GEO) GEN HOSPITAL CORP.
PA	(FARB) BAYER AG.
PA	
PI	Woolf C, D'urso D, Befort K, Costigan M;
XX	
XX	WFI; 2003-268312/26.
DR	
DR	GENBANK; NP_004655.
XX	
PT	New composition comprising two or more isolated polypeptides, u
PT	preparing a medicament for treating pain in an animal.
PT	
PS	Claim 1; Page: 1017pp; English.
PS	

Claim 1: Page: 1017pp: English.

The invention discloses a composition comprising two or more isomers or human polynucleotides or a polynucleotide which represents a derivative or allelic variation of the nucleic acid sequence. A polynucleotide is a sequence of nucleotides. A polynucleotide is claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence, a method for identifying a polynucleotide sequence, a method which is differentially regulated in an animal subjected to pain, a kit to perform the method, an array, a method for identifying a polynucleotide sequence, a method for identifying a polynucleotide sequence that increases or decreases the expression of the polynucleotide that is differentially expressed in neuronal tissue of a first animal, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition for identifying a compound or small molecule that regulates the activity of one or more of the polynucleotides given in an animal, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound modulates its activity is useful for preparing a medicament for the treatment of pain (e.g. spinal segmental nerve injury (Chung)), chronic constipation (e.g. spinal segmental nerve injury (SNI)), chronic constipation (CCI) and spared nerve injury (SNI)) in an animal (e.g. rat, mouse, monkey, human). The sequence presented is a human protein (shown in Table 1) which is differentially expressed during pain. The sequence data for this patent did not form part of the prior art. The sequence data was obtained in electronic form directly from the following website: <http://www.ncbi.nlm.nih.gov/ftgwipo.int/pub/published.pct.sequences>.

Sequence 233 AA:

Query Match	100.0%	Score 1170;	DB 7;	Length 233;
Best Local Similarity	100.0%;	Pred. No. 7.5e-108;		
Matches 233;	Conservative 0;	Mismatches 0;	Indels 0;	

Qy	1	MLKPSVTSAPTDAMATLTVVQPLFLDIDVARAIELLEKLQBSGEVPPVHKLQSLK
Db	1	MLKPSVTSAPTDAMATLTVVQPLFLDIDVARAIELLEKLQBSGEVPPVHKLQSLK
Qy	61	FTATREVVQYMHETTIVNGCPEFRABATATAKATAFAASGSHSHPRVVELPKT
Db	61	FTATREVVQYMHETTIVNGCPEFRABATATAKATAFAASGSHSHPRVVELPKT
Qy	121	NWGGKQNSPIYISRIIPGGVABRHGGLKRGDQLLSNVGVSVEGEHHEKAVEL
Db	121	NWGGKQNSPIYISRIIPGGVABRHGGLKRGDQLLSNVGVSVEGEHHEKAVEL
Qy	181	SVKLVRYTPKV-EEMEARFEKLTARRRROOOLLITOOOOCOCOCOCOTOOHMS

all growth factor activity, haematopoiesis regulating
issue growth factor activity, immunomodulatory activity and
in activity and may be useful in the diagnosis and/or
f cancer, leukaemia, nervous system disorders, arthritis and
n. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
and 3666 (AAM80020) are omitted as the relevant pages from the
sing were missing at the time of publication

7 AA;

69.6%; Score 814; DB 4; Length 197;

ilarity 80.6%; Pred. No. 1.6e-72;

Conservative 24; Mismatches 13; Indels 0; Gaps 0;

LTLDRVARALELLEKLGSGEVPVHKLQSLKXKLVQSEFCTAIREVVOYMHETIIVNG 80
VLELDRICRALELLEKLGSGEVPVHKLQSLKXKLVQSEFCTAIREVVOYMHETIIVNG 80
VLELDRICRALELLEKLGSGEVPVHKLQSLKXKLVQSEFCTAIREVVOYMHETIIVNG 80

EFPRATATATVAAPAAAGSHSHPRVVELPKTDEGLGFGNVGKGKQNSPIYISRIIPG 140
SVRANATATATVAAPAAAGSHSHPRVVELPKTDEGLGFGNVGKGKQNSPIYISRIIPG 140
SVRANATATATVAAPAAAGSHSHPRVVELPKTDEGLGFGNVGKGKQNSPIYISRIIPG 140

AFRHGGLKRGDQLLSVNGSVGEHHEKAVELLKAAKDSVKLVVRYTPKVLSEMEARF 200
ADRHGGLKRGDQLLSVNGSVGEHHEKAVELLKAAKDSVKLVVRYTPKVLSEMEARF 200
ADRHGGLKRGDQLLSVNGSVGEHHEKAVELLKAAKDSVKLVVRYTPKVLSEMEARF 200

XTARRRQQ 211
MESAKRRQQ 196

andard; protein; 197 AA.

(first entry)

in sequence SEQ ID NO:13038.

ar; detection; diagnosis; antisense therapy; gene therapy.

3.

2.

2000EP-00116126.

99JP-00248036.

99JP-00300253.

2000JP-00118776.

2000JP-00183767.

2000JP-00241899.

EX RES INST.

rai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
giyama T, Wakamatsu A, Nagai K, Otsuki T;

18749/34.

for synthesizing polynucleotides, particularly the 5602 full-
s defined in the specification, and for the detection and/or
s the abnormality of the proteins encoded by the full-length

ID NO 13038; 2537pp + Sequence Listing; English.

vention describes primer sets for synthesising 5602 full-
s defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to
complementary strand of a polynucleotide which comprises one of
nucleotide sequences defined in the specification, where the
oligonucleotide comprises at least 15 nucleotides; or (b) a com
of an oligonucleotide comprising a sequence complementary to th
complementary strand of a polynucleotide which comprises a 5'-e
sequence and an oligonucleotide comprising a sequence complemen
polynucleotide which comprises a 3'-end sequence, where the
oligonucleotide comprises at least 15 nucleotides and the combi
the 5'-end sequence/3'-end sequence is selected from those defi
specification. The primer sets can be used in antisense therapy
gene therapy. The primers are useful for synthesising polynucle
particularly full-length cDNAs. The primers are also useful for
detection and/or diagnosis of the abnormality of the proteins e
the full-length cDNAs. The primers allow obtaining of the full-
cDNAs easily without any specialised methods. AAH03166 to AAH13
AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 t
represent human amino acid sequences; and AAH13629 to AAH13632
oligonucleotides, all of which are used in the exemplification
present invention
XX Sequence 197 AA;

Query Match 69.6%; Score 814; DB 4; Length 197;
Best Local Similarity 80.6%; Pred. No. 1.6e-72;
Matches 154; Conservative 24; Mismatches 13; Indels 0;

QY 21 QPLTLDRVARALELLEKLGSGEVPVHKLQSLKXKLVQSEFCTAIREVVOYMH
Db 6 EPVLERDICRALELLEKLGSGEVPVHKLQSLKXKLVQSEFCTAIREVVOYMH

QY 81 CPEFRATATATVAAPAAAGSHSHPRVVELPKTDEGLGFGNVGKGKQNSPIYI
Db 66 SPEVRANATATATVAAPAAAGSHSHPRVVELPKTDEGLGFGNVGKGKQNSPIYI

QY 141 GVAERHGLKRGDQLLSVNGSVGEHHEKAVELLKAAKDSVKLVVRYTPKVL
Db 126 GIADRHGGLKRGDQLLSVNGSVGEHHEKAVELLKAAKDSVKLVVRYTPKVL

QY 201 EKLRTARRRQQ 211
Db 186 EKRSAKRRQQ 196

RESULT 8

AAM79876

ID AAM79876 standard; protein; 198 AA.

XX AAM79876;

XX 06-NOV-2001 (first entry)

XX Human protein SEQ ID NO 3522.

XX Human; cytokine; cell proliferation; cell differentiation; gene
vaccine; peptide therapy; stem cell growth factor; haematopoies
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation.

XX Homo sapiens.

XX WO200157190-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US004098.

XX 03-FEB-2000; 2000US-00496914.

XX 27-APR-2000; 2000US-00560875.

XX 20-JUN-2000; 2000US-00598075.

XX 19-JUL-2000; 2000US-00620325.

XX 01-SEP-2000; 2000US-00654936.

XX 15-SEP-2000; 2000US-00663561.

us-09-909-005-1.rag

cellular matrix and cell adhesion molecule; XMAP; genetic disorder; adrenoleukodystrophy; leukoemia; disease; cystic fibrosis; Gaucher's disease; myotonic dystrophy; anaemia; thalassemia; autoimmune disorder; adenocarcinoma; disorder; acquired immune deficiency syndrome; AIDS; disease; allergy; anaemia; asthma; atherosclerosis; melanoma; disease; diabetes mellitus; atopic dermatitis; lymphoma; cancer; arthritis; multiple sclerosis; Grave's disease; osteoarthritis; psoriasis; rheumatoid arthritis; ulcerative colitis;

enoyers L, Gerritsen ME, Goddard A, Godowski PJ;
Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
2045/32.
5878.

and twenty two nucleic acids encoding PRO polypeptides,
he manufacture of a medicament for diagnosing or treating

g 76; 314pp; English.

invention relates to the isolation of novel human PRO
, and the polynucleotide sequences encoding them. The PRO
are secreted and transmembrane proteins. The PRO
and polynucleotides are useful for preparing a medicament
e diagnosis and treatment of tumours. Anti-PRO antibodies are
agnostic assays for PRO, by detecting its expression in
is, tissues or serum, and for affinity purification of PRO
nant cell culture or natural sources. AB080739-AB080860
e human PRO polypeptides of the invention. Note: The sequence
s patent was obtained in electronic format directly from the
te at seqdata.uspto.gov/psipspIDentry.html

AA;

69.0%; Score 807; DB 6; Length 207;

larity 78.5%; Pred. No. 8.4e-72;

Conservative 24; Mismatches 17; Indels 2; Gaps 1;

LTVQPLTDRDVARAIELEKLEQSEGEVPHVKLSKLVQSEFCTATREVVQYMH 73

L--VEPLGLEDVDSRAVELLERLQSGELPPKQLQALQVLRFCSAIREVQILY 58

TNGCPEPRATATKATAFAASEGSHSPRVVLPKTDGLGFNVNGKQNSPIY 133

DITGSAETRAHATAKATAFAASEGSHSPRVVLPKTDGLGFNVNGKQNSPIY 118

IIPGGVAERHGLKRGDQLLSVNGSVSEGEHHEKAVELLKAAKDSVKLVVTPKVL 193

VIPGGVADRHGGLKRGDQLLSVNGSVSEGEHHEKAVELLKAAQGSVKLVVTPKVL 178

EARFEKLTARRRQQQQ 213

|||||:|||||

EARFEKMSRSARRQQHQ 198

ndard; protein; 207 AA.

(first entry)

secreted and transmembrane protein PRO10200.

ted and transmembrane protein; PRO; cytostatic;
c; osteopathic; gene therapy; TNF-Agonist-Alpha;
stimulator; pericyte stimulator; fibroblast modulator;
al; diagnostic; biosensor; bioresactor; tumour; lung tumour;
; breast tumour; prostate tumour; rectal tumour;
; bone disorder; cartilage disorder; sports injury;
ound.

-Al.

2002US-00218631.

XX

PR 01-JUN-2001; 2001WO-US017800.

PR 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, W

XX MPI; 2003-512315/48.

DR N-PSDB; ACD68630.

XX New genes, and its encoded secreted and transmembrane polypeptid

PT useful for stimulating tumor Necrosis Factor alpha, or chondrocy

PT pericyte proliferation, especially for treating lung tumors, art

XX wounds in a mammal.

Claim 11; Fig 76; 314pp; English.

CC The invention describes an isolated nucleic acid molecule compri

CC sequence with at least 80% identity to: (a) a nucleotide encodin

CC 122 PRO (secreted and transmembrane) polypeptides whose sequenc

CC fully defined in the specification; or (b) any of 122 nucleotide

CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the

CC specification; or the full length coding sequence of any these 1

CC nucleotide sequences. The PRO polypeptides or polynucleotides ar

CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These

CC particularly useful for detecting tumours (e.g. lung tumour, col

CC tumour, breast tumour, prostate tumour, rectal tumour, or liver

CC in a mammal, for stimulating the release of TNF-alpha from human

CC cells for stimulating the proliferation or differentiation of chondro

CC normal human dermal fibroblast proliferation. The PRO nucleic ac

CC polypeptide is also useful for treating tumours or various bone

CC cartilage disorders (e.g. sports injuries or arthritis), or woun

CC PRO polypeptides are useful in drug screening, particularly as t

CC for therapeutic intervention in these diseases, and in the diagn

CC determination of the presence of these diseases. The PRO polypep

CC also useful as molecular weight markers, or for chromosome

CC identification. The PRO genes are useful as hybridisation probes

CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO

CC also be used in gene therapy, particularly for replacing a defec

CC gene. This is the amino acid sequence of a novel human secreted

CC transmembrane PRO polypeptide

XX Sequence 207 AA;

SQ Query Match 69.0%; Score 807; DB 6; Length 207;

Best Local Similarity 78.5%; Pred. No. 8.4e-72;

Matches 157; Conservative 24; Mismatches 17; Indels 2;

QY 14 MALTIVVQPLTDRDVARAIELEKLEQSEGEVPHVKLSKLVQSEFCTATREVV

Db 1 MAAL--VEPLGLEDVDSRAVELLERLQSGELPPKQLQALQVLRFCSAIREV

QY 74 ETTIVNGCPEPRATATKATAFAASEGSHSPRVVLPKTDGLGFNVNGKQEQ

Db 59 DTDITGSAETRAHATAKATAFAASEGSHSPRVVLPKTDGLGFNVNGKQEQ

QY 134 ISRIIPGGVAERHGLKRGDQLLSVNGSVSEGEHHEKAVELLKAAKDSVKLVVRY

Db 119 ISRVIPGGVADRHGGLKRGDQLLSVNGSVSEGEHHEKAVELLKAAQGSVKLVRY

QY 194 EMEARFEKLTARRRQQQQ 213

Db 179 EMEARFEKMSRSARRQQHQ 198

RESULT 13

AB082085

ID AB082085 standard; protein; 207 AA.

XX

us-09-909-005-1.rag

[illegible]

15:31:25 2004

us-09-909-005-1.rag

VTGGVADRHGGLKRGDQLLSVNGSVGEQHEKAVELLKAAQSSVKNVRYTPRVL 178

SARFEKLTARRRQQQ 213

SARFEKNSARRRQQHQ 198

adard; protein; 207 AA.

(first entry)

30 protein.

proliferation; pericyte cell; TNF alpha; chondrocyte;
sis factor; proliferation; differentiation; gene therapy;
blast.

-A1.

2002US-00227884.

2001WO-US017800.

2001WO-US021066.

2002US-00119480.

VTECH INC.

senoyers L, Gerritsen ME, Goddard A, Godowski PJ;
Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
3301/47.
4546.

sin encoding nucleic acid, useful for preparing PRO
and anti-PRO antibodies for detecting the presence of a
animal.

3 76; 324pp; English.

a relates to a novel isolated PRO protein encoding nucleic
acid of the invention may be useful for preparing PRO
and anti-PRO antibodies for detecting the presence of a
animal. Furthermore, the molecules of the invention may be
stimulating proliferation or gene expression in pericyte
release of tumour necrosis factor (TNF)-alpha from human
roliferation or differentiation of chondrocyte cells and for
he proliferation of normal human dermal fibroblast cells.
molecules may be utilised during gene therapy. The current
that of the human PRO protein of the invention

AA;

69.0%; Score 807; DB 6; Length 207;

larity 78.5%; Pred. No. 8.4e-72;

Conservative 24; Mismatches 17; Indels 2; Gaps 1;

LTVVQPLDRDVARAIELLEKLOESGEVPHVKLSLKKVLQSEFCTAIREVYQTMH 73

L--VEPLGLERDVSRAVELLRELQSGELPPQKLQALQRLQSFQCSAIREVEQLY 58

TVNGCPERARATAKATVAFAASEGSHSRVVELPKTDEGLGNVNGGKQNSPIY 133

DITGSAETRAHATAKATAAFTASEGHAHPRVVELPKTDEGLGNMGKQNSPIY 118

IIPGGVABRHGGLKRGDQLLSVNGSVGEQHEKAVELLKAAKDSVKLVVRYTPKVL 193

Db 119 ISRVIPGGVADRHGGLKRGDQLLSVNGSVGEQHEKAVELLKAAQSSVKNVRY

QY 194 EMEARFEKLTARRRQQQ 213

Db 179 EMEARFEKNSARRRQQHQ 198

Search completed: March 18, 2004, 13:26:52

Job time : 61 secs

15:31:25 2004

us-09-909-005-1.rapb

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

ein search, using sw model

arch 18, 2004, 13:28:25 ; Search time 42 Seconds
(without alignments)
1436.586 Million cell updates/sec

S-09-909-005-1

170 MLKPSVTSAPTADMATLVV.....LLIQQQQQQQQQTQQNHS 233

LOSJM62

apoc 10.0 , Gapext 0.5

.049977 seqs, 258955339 residues

its satisfying chosen parameters: 1049977

length: 0

length: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Published Applications AA:*

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2: /cgn2_6/ptodata/2/pubaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubaa/US10B_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep.*

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

Query Match	Length	DB	ID	Description
100.0	233	9	US-09-909-005-1	Sequence 1, Appl
69.0	207	12	US-10-219-535-76	Sequence 76, Appl
69.0	207	12	US-10-232-230-76	Sequence 76, Appl
69.0	207	14	US-10-227-884-76	Sequence 76, Appl
69.0	207	14	US-10-230-163-76	Sequence 76, Appl
69.0	207	14	US-10-149-819-19	Sequence 19, Appl
69.0	207	14	US-10-230-338-76	Sequence 76, Appl
69.0	207	14	US-10-218-631-76	Sequence 76, Appl
69.0	207	14	US-10-230-414-76	Sequence 76, Appl
69.0	207	14	US-10-216-159A-76	Sequence 76, Appl
69.0	207	14	US-10-218-849-76	Sequence 76, Appl
69.0	207	14	US-10-227-873-76	Sequence 76, Appl
69.0	207	14	US-10-227-883-76	Sequence 76, Appl
69.0	207	14	US-10-219-076-76	Sequence 76, Appl
69.0	207	14	US-10-230-434-76	Sequence 76, Appl

16	807	69.0	207	14	US-10-219-003-76	Sequence
17	807	69.0	207	14	US-10-219-075-76	Sequence
18	807	69.0	207	14	US-10-219-464-76	Sequence
19	807	69.0	207	14	US-10-219-466-76	Sequence
20	807	69.0	207	14	US-10-219-479-76	Sequence
21	807	69.0	207	14	US-10-219-481-76	Sequence
22	807	69.0	207	14	US-10-230-260-76	Sequence
23	807	69.0	207	14	US-10-232-231-76	Sequence
24	807	69.0	207	14	US-10-232-233-76	Sequence
25	807	69.0	207	14	US-10-216-165-76	Sequence
26	807	69.0	207	14	US-10-218-956-76	Sequence
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41	807	69.0	207	14	US-10-232-225-76	Sequence
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43	807	69.0	207	14	US-10-232-229-76	Sequence
44	807	69.0	207	14	US-10-232-234-76	Sequence
45	807	69.0	207	14	US-10-219-060-76	Sequence

ALIGNMENTS

RESULT 1
US-09-909-005-1
; Sequence 1, Application US/09909005
; Patent No. US20020082388A1
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: CELL JUNCTION PDZ PROTEIN
; FILE REFERENCE: PF-0599 US
; CURRENT APPLICATION NUMBER: US/09/309,005
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/370,1
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-06
; SOFTWARE: PERL Program
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 1
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1974337
US-09-909-005-1

Query Match 100.0%; Score 1170; DB 9; Length 233;
Best Local Similarity 100.0%; Pred. No. 4.2e-105;
Matches 233; Conservative 0; Mismatches 0; Indels 0;

QY 1 MLKPSVTSAPTADMATLVVQPLTLDROVARATELLEKIQESGVPVHKQSLK
DB 1 MLKPSVTSAPTADMATLVVQPLTLDROVARATELLEKIQESGVPVHKQSLK
QY 61 FCTAIREVYQMHETITVNGCPEFRARATATVAFAASEGSHSHPRVVELPKT
DB 61 FCTAIREVYQMHETITVNGCPEFRARATATVAFAASEGSHSHPRVVELPKT
QY 121 NVWGKQNSPIYTSRIIPGVAERHGLKRGDQLLSVNGSVSGEHHKAVEL

15:31:25 2004

us-09-909-005-1.rapb

3KEQNSPIYISRIIPGGVAERHGLKRGDQLLSVNGSVGEHEKAVELLKAAKD 180
JVRYTPKVLBNARFKLRTARRRQOOQLLIQOOOQOOOQOOQOOQNHMS 233
JVRYTPKVLBNARFKLRTARRRQOOQLLIQOOOQOOOQOOOQOOQNHMS 233
plication US/10219535
US20040044179A1
TION:
er, Kevin P.
snoyers, Luc
rritsen, Mary
daard, Audrey
Jowski, Paul J.
imaldi, J. Christopher
rney, Austin L.
ith, Victoria
ephan, Jean-Philippe F.
tanabe, Colin L.
od, William I.
TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TION: ACIDS ENCODING THE SAME
: P3530P1C60
ATION NUMBER: US/10/219,535
DATE: 2002-08-14
ION NUMBER: 10/119,480
ATE: 2002-04-09
ION NUMBER: 60/059113
ATE: 1997-09-17
ION NUMBER: 60/062287
ATE: 1997-10-17
ION NUMBER: 60/063549
ATE: 1997-10-28
ION NUMBER: 60/064103
ATE: 1997-10-31
ION NUMBER: 60/069873
ATE: 1997-12-17
ION NUMBER: 60/078910
ATE: 1998-03-20
ION NUMBER: 60/079294
ATE: 1998-03-25
ION NUMBER: 60/079656
ATE: 1998-03-26
ION NUMBER: 60/079728
ATE: 1998-03-27
r Application data removed - See File Wrapper or PALM.
ID NOS: 246
o Sapien
69.0%; Score 807; DB 12; Length 207;
larity 78.5%; Pred. No. 5.5e-70;
Conservative 24; Mismatches 17; Indels 2; Gaps 1;
LTVVQPLTLDRDVARAIELEKIQSGEVPVHKQLSKLVQSEFCTAIREVYQWH 73
L--VEPLGLERDVSRAVELLERLQSGELPPQKLOALQRLVQSRFCSAIREV 58
TVNGCEFRATATKATVAAPAAASGHSHPRVVELPKTDEGLGNNVGGKQNSPIY 133
DITGSAETRAHATATKATVAAPTASGHHAHPRVVELPKTDEGLGNNVGGKQNSPIY 118
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FEARFKLRTARRRQOOQ 213

Db 179 EEMEARFEKMSARRRQHQ 198
RESULT 3
US-10-232-230-76
; Sequence 76, Application US/10232230
; Publication No. US20040044180A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Matanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NU
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C103
; CURRENT APPLICATION NUMBER: US/10/232,230
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PAL
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 76
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-232-230-76
Query Match 69.0%; Score 807; DB 12; Length 207;
Best Local Similarity 78.5%; Pred. No. 5.5e-70;
Matches 157; Conservative 24; Mismatches 17; Indels 2;
Qy 14 MATITVVQPLTLDRDVARAIELEKIQSGEVPVHKQLSKLVQSEFCTAIREV
Db 1 MAAL--VEPLGLERDVSRAVELLERLQSGELPPQKLOALQRLVQSRFCSAIREV
Qy 74 ETTIVNGCEFRATATKATVAAPAAASGHSHPRVVELPKTDEGLGNNVGGKQ
Db 59 DLTIDTGSATRAHATATKATVAAPTASGHHAHPRVVELPKTDEGLGNNVGGKQ
Qy 134 ISRIIPGGVAERHGLKRGDQLLSVNGSVGEHEKAVELLKAAKDSKLVVRY
Db 119 ISRVIPGGVADHGLKRGDQLLSVNGSVGEHEKAVELLKAAQGSVKLVVRY
Qy 194 EEMEARFEKLTARRRQOOQ 213
Db 179 EEMEARFEKMSARRRQHQ 198

plication US/10227884
US20030027988A1
TION:
ar, Kevin P.
shoyers, Luc
ritsen, Mary
ddard, Audrey
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inaldi, J. Christopher
mey, Austin L.
ich, Victoria
ephan, Jean-Philippe F.
tanabe, Colin L.
od, William I.
TION: ACIDS ENCODING THE SAME
: P3530P1C79
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ATE: 1999-12-07
ION NUMBER: 60/169835

69.08; Score 807; DB 14; Length 207;

larity 78.5%; Pred. No. 5.5e-70;
Conservative 24; Mismatches 17; Indels 2; Gaps 1;

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.DITGSAEIRAHATAKATAAFTASEGHAHPRVVELPKTDEGLFNVMGKQNSPIY 118

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:VIFPGVADRHGLKRGDQLLSVNGSVSVEGEHKAVALLEKAAKOSVKLVRYTPRVL 178

QY 194 EWEARFEKLTARRRQQOQ 213
Db 179 EWEARFEWMSARRRQQHQ 198

RESULT 5

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; Publication No. US20030036635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Destoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NU
; FILE REFERENCE: P3530P1C96
; CURRENT APPLICATION NUMBER: US/10/230,163
; CURRENT FILING DATE: 2002-08-28
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PRIOR APPLICATION NUMBER: 60/169835

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QY 74 EITVNGCPFRARATKATVAFAASEGSHSHPVVELPKTDEGLGNVMGCKE

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TION:
YTE GENOMICS, INC.
E, Henry
IMZAI, Yalda
NG, Y. Tom
TTERSON, Chandra
UGHN, Mariah R.
, Dyung Aina M.
AH, Purvi
L, Preeti
-YOUNG, Janice
RFORD, Neil
TION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
: PF-0760 PCT
ATION NUMBER: US/10/149,819
DATE: 2002-06-10
ION NUMBER: 60/172,852; 60/172,354
ATE: 1999-12-10; 1999-12-16
ID NOS: 42
Program

o sapiens
c.feature
TION: Incyte ID No. US20030044913A1 4062841CD1

69.0%; Score 807; DB 14; Length 207;
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er, Kevin P.
enoyers, Luc
eritsen, Mary

APPPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Matanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMERANE POLYPEPTIDES AND NU
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
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; PRIOR FILING DATE: 1998-03-27
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; NUMBER OF SEQ ID NOS: 246
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-338-76

Query Match 69.0%; Score 807; DB 14; Length 207;
Best Local Similarity 78.5%; Pred. No. 5.5e-70;
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Db 59 DTLDTGSAETRAHATAKATAVAFTASEGHAHPRVVVELPKTDEGLGFMNGKQNS
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Db 119 ISRVIPGVADRHGGKRGDQLLSVNGSVSEGEHHEKAVELLKAAKDSVKLVVR
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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us-09-909-005-1.rapb

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rney, Austin L.
ith, Victoria
ephan, Jean-Philippe F.
tanabe, Colin L.
od, William I.
TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TION: ACIDS ENCODING THE SAME
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ID NOS: 246

o Sapien
69.0%; Score 807; DB 14; Length 207;
larity 78.5%; Pred. No. 5.5e-70;
Conservative 24; Mismatches 17; Indels 2; Gaps 1;

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er, Kevin P.
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ddard, Audrey
dowski, Paul J.
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ith, Victoria
-ephan, Jean-Philippe F.

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; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NI
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; ORGANISM: Homo Sapien
US-10-230-414-76

Query Match 69.0%; Score 807; DB 14; Length 207;
Best Local Similarity 78.5%; Pred. No. 5.5e-70;
Matches 157; Conservative 24; Mismatches 17; Indels 2;

Qy 14 MATLVVQPLTDRVARALELLEKLOESGVPVHKVLSKVLQSEFCTAIREY
Db 1 MAAL--VEPLGLERDVSRAVELLERLQSGELPPKQLQALQRLVLSRFSALIREY
Qy 74 ETIVNGCPFRATATKATVAAPAAASEGSHPRVVELPKTDGLGPNVVGKEK
Db 59 DITGSAEIRAHATAKATVAAPAAASEGSHPRVVELPKTDGLGPNVVGKEK
Qy 134 ISRIIPGVVAERHGLKRGDQLLSVNGSVSVEGEHEKAVELLKAAKDSVLYTPKVL
Db 119 ISRVIPGVVADRHGGLKRGDQLLSVNGSVSVEGEHEKAVELLKAAKDSVLYTPKVL
Qy 194 BEMEARFEKLTARRRQQQ 213
Db 179 BEMEARFEKLTARRRQQH 198

RESULT 10
US-10-216-159A-76
; Sequence 76, Application US/10216159A
; Publication No. US20030069397A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NI
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15:31:25 2004

us-09-909-005-1.rapb

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; ION: ACIDS ENCODING THE SAME
; P3530P1C6
; ATION NUMBER: US/10/216,159A
; DATE: 2002-08-09
; ION NUMBER: 10/119,480
; ATE: 2002-04-09
; ION NUMBER: 60/059113
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; ION NUMBER: 60/062287
; ATE: 1997-10-17
; ION NUMBER: 60/063549
; ATE: 1997-10-28
; ION NUMBER: 60/064103
; ATE: 1997-10-31
; ION NUMBER: 60/069873
; ATE: 1997-12-17
; ION NUMBER: 60/078910
; ATE: 1998-03-20
; ION NUMBER: 60/079294
; ATE: 1998-03-25
; ION NUMBER: 60/079656
; ATE: 1998-03-26
; ION NUMBER: 60/079728
; ATE: 1998-03-27
; Application data removed - See File Wrapper or PALM.
; ID NOS: 246

; Sapien

69.0%; Score 807; DB 14; Length 207;
arity 78.5%; Pred. No. 5.5e-70;
onservative 24; Mismatches 17; Indels 2; Gaps 1;

; TVVQPLTDRDVARAIELLEKLOESGEVPHVKLOSLKVLQSEFCTAIREVQYMH 73
; --VEPLGLERDVSRVAVELLERLQSGELPPQKLOALQORVLQSFCSAIREVQY 50
; TVNGCPFRARATATAVAFAASEGHSHPRVVELPKTDEGLGNFMVWGKQNSPIY 133
; ITGSAEIRAHATAKATVAFTAASEGHAHPRVVELPKTDEGLGNFMVWGKQNSPIY 118
; IIPGVARHGGLKGDQLLSVNGSVSGEHEKAVELLKAAKDSVKLVVRYTPVL 193
; IIPGVADRHGGLKGDQLLSVNGSVSGEHEKAVELLKAAQGSVKLVVRYTPVL 178
; ARFEKLTARRRQOOQ 213
; ARFEKWSARRRQOQ 198

; Application US/10218849
; US20030073814A1
; ION:
; ar, Kevin P.
; snoyers, Luc
; critsen, Mary
; idard, Audrey
; lowski, Paul J.
; imaldi, J. Christopher
; ney, Austin L.
; ith, Victoria
; sphan, Jean-Philippe F.
; -anabe, Colin L.
; od, William I.
; ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ION: ACIDS ENCODING THE SAME
; : P3530P1C11
; ATION NUMBER: US/10/218,849
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; CURRENT FILING DATE: 2002-08-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 76
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-218-849-76

Query Match 69.0%; Score 807; DB 14; Length 207;
Best Local Similarity 78.5%; Pred. No. 5.5e-70;
Matches 157; Conservative 24; Mismatches 17; Indels 2;

QY 14 MATLVQPLTDRDVARAIELLEKLOESGEVPHVKLOSLKVLQSEFCTAIREV
Db 1 MAAL--VEPLGLERDVSRVAVELLERLQSGELPPQKLOALQORVLQSFCSAIREV
QY 74 ETITVNGCPFRARATATAVAFAASEGHSHPRVVELPKTDEGLGNFMVWGKQEQ
Db 59 DTLDTGSAEIRAHATAKATVAFTAASEGHAHPRVVELPKTDEGLGNFMVWGKQEQ
QY 134 ISRIIPGVARHGGLKGDQLLSVNGSVSGEHEKAVELLKAAKDSVKLVVRY
Db 119 ISRVIPGVADRHGGLKGDQLLSVNGSVSGEHEKAVELLKAAQGSVKLVVRY
QY 194 EMEARFEKLTARRRQOOQ 213
Db 179 EMEARFEKWSARRRQOQ 198

RESULT 12
US-10-227-873-76
; Sequence 76, Application US/10227873
; Publication No. US20030073816A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
; FILE REFERENCE: P3530P1C72
; CURRENT APPLICATION NUMBER: US/10/227,873
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
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; PRIOR FILING DATE: 1997-10-31
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; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
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; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
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ON NUMBER: 60/084441
ATE: 1998-05-06
ON NUMBER: 60/085323
ATE: 1998-05-13
ON NUMBER: 60/085579
ATE: 1998-05-15
ON NUMBER: 60/086392
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ON NUMBER: 60/089532
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ON NUMBER: 60/090691
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PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320
PRIOR FILING DATE: 1999-08-17

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PRIOR FILING DATE: 1998-03-26
 PRIOR APPLICATION NUMBER: 60/079728
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PRIOR FILING DATE: 1998-06-25

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PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812

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PRIOR APPLICATION NUMBER: 60/099816

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PRIOR APPLICATION NUMBER: 60/100038

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PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101477

PRIOR FILING DATE: 1998-09-23

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; PRIOR FILING DATE: 1999-07-28
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; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
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; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match          69.0%; Score 807; DB 14; Length 207;
Best Local Similarity 78.5%; Pred. No. 5.Se-70;
Matches 157; Conservative 24; Mismatches 17; Indels 2;

QY 14 MATLTVQPTLDRVARAIELLEKLOESCEYVPHKLOSLKKVLQSEFCTAIRE
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MAAL--VEPLGLERDVSRAVELLERLQRSGLPQKQLQRLQSRFCSAIRE

QY 74 EITVWGCPFRARATAKATVAATAASEGSHPRVVELPKTDEGLGFNVWGCKE
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59 DTLDTISAIRAHATAKATVAATASEGHAPRVVELPKTDEGLGFNVWGCKE

QY 134 ISRIIPGVSAERHGG:KRGDQLLSVNGSVSVEGHEHEKAVELLKAAKDSVKLVVR
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 119 ISRVIPGVADRHGG:KRGDQLLSVNGSVSVEGHEKAVELLKAAQGSVKLVVR

QY 194 EMEARPEKLTARRRQOOQ 213
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 EMEARPEKMSARRRQHQ 198

RESULT 14
US-10-219-076-76
; Sequence 76, Application US/10219076
; Publication NO. US20030078379A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND N
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C62
; CURRENT APPLICATION NUMBER: US/10/219,076
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
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7 PRIOR FILING DATE: 1998-03-25
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8	PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090557
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Qy	74	EITITVNGCPFRARATAKATVAFAASGESHSPRVVELPKTDEGLGNVMGCKE
Db		59 DTLDTITGSAEIRAHATAKTVAATFASGEHAHPRVVELPKTDEGLGNIMGCKE
Qy	134	ISRIIPGVAERHGGIKRGDQLLSVNGSVSYEGEHBHEKAVELLKAAKOSVKLVVR
Db		119 ISRVIPGVAERHGGIKRGDQLLSVNGSVSYEGEHBHEKAVELLKAAQOSVKLVVR
Qy	194	EMEARPFKLTARREQQQQ 213
Db		179 EMEARPFKNSRRRROOHC 198

Search completed: March 18, 2004, 13:34:03
Job time : 43 secs

15:31:25 2004

us-09-909-005-1.ra1

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ein search, using sw model

March 18, 2004, 13:25:44 ; Search time 23 Seconds
(without alignments)

522.994 Million cell updates/sec

IS-09-909-005-1

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ILOSUM62

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189414 seqs, 51625971 residues

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length: 0

length: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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:/cgn2_6/ptodata/2/iaa/6AC_COMB.pep.*

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:/cgn2_6/ptodata/2/iaa/6AN_COMB.pep.*

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er than or equal to the score of the result being printed,
ved by analysis of the total score distribution.

SUMMARIES

Query	Length	DB	ID	Description
00.0	233	2	US-09-151-611-1	Sequence 1, Appli
00.0	233	3	US-09-370-102-1	Sequence 1, Appli
55.0	297	2	US-09-151-611-3	Sequence 3, Appli
55.0	297	3	US-09-370-102-3	Sequence 3, Appli
16.8	724	4	US-09-562-737-21	Sequence 21, Appli
16.2	1881	4	US-09-233-086-3	Sequence 3, Appli
15.7	2465	2	US-08-596-291-3	Sequence 3, Appli
15.7	2465	3	US-09-100-804-3	Sequence 3, Appli
15.4	724	4	US-09-562-737-30	Sequence 30, Appli
15.4	2466	3	US-09-080-855-12	Sequence 12, Appli
15.4	2466	4	US-09-566-076-12	Sequence 12, Appli
15.4	2466	5	PCT-US94-09943-2	Sequence 2, Appli
14.9	2037	3	US-09-306-998-3	Sequence 3, Appli
14.8	724	4	US-09-562-737-27	Sequence 27, Appli
14.7	77	3	US-09-100-804-16	Sequence 16, Appli
14.7	724	4	US-09-562-737-28	Sequence 28, Appli
14.6	724	4	US-09-562-737-23	Sequence 23, Appli
14.6	80	3	US-08-545-860D-54	Sequence 54, Appli
14.6	80	5	PCT-US94-04496-54	Sequence 54, Appli
14.4	2485	3	US-09-290-640-46	Sequence 46, Appli
14.4	2485	4	US-09-663-615B-46	Sequence 46, Appli
14.4	724	4	US-09-562-737-29	Sequence 29, Appli
14.1	724	4	US-09-562-737-26	Sequence 26, Appli
13.8	724	4	US-09-562-737-25	Sequence 25, Appli
13.5	206	4	US-09-562-737-51	Sequence 51, Appli
13.4	73	3	US-09-100-804-28	Sequence 28, Appli
13.4	610	1	US-08-410-804-1	Sequence 1, Appli

28	156.5	13.4	610	1	US-08-259-514-1	Sequence
29	156.5	13.4	610	2	US-08-858-311-1	Sequence
30	155.5	13.3	73	3	US-09-100-804-25	Sequence
31	155	13.2	374	3	US-09-091-405-2	Sequence
32	155	13.2	631	4	US-09-147-119-7	Sequence
33	151.5	12.9	77	3	US-09-100-804-17	Sequence
34	149.5	12.8	724	4	US-09-562-737-24	Sequence
35	148.5	12.7	724	4	US-09-562-737-22	Sequence
36	147.5	12.6	206	4	US-09-562-737-56	Sequence
37	147.5	12.6	505	1	US-08-123-161A-14	Sequence
38	147.5	12.6	505	1	US-08-483-278-14	Sequence
39	146	12.5	632	4	US-09-976-594-41	Sequence
40	145.5	12.4	206	4	US-09-562-737-52	Sequence
41	145	12.4	358	4	US-09-740-027-4	Sequence
42	143.5	12.3	79	3	US-09-100-804-27	Sequence
43	143.5	12.3	86	3	US-08-545-860D-53	Sequence
44	143.5	12.3	86	5	PCT-US94-04496-53	Sequence
45	142.5	12.2	249	4	US-09-673-395A-338	Sequence

ALIGNMENTS

RESULT 1
US-09-151-611-1
; Sequence 1, Application US/09151611
; Patent No. 5958731
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: CELL JUNCTION PDZ PROTEIN
; FILE REFERENCE: PF-0599 US
; CURRENT APPLICATION NUMBER: US/09/151,611
; CURRENT FILING DATE: 1998-09-11
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1974337
US-09-151-611-1

Query Match 100.0%; Score 1170; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 2.5e-109;
Matches 233; Conservative 0; Mismatches 0; Indels 0;
Qy 1 MKPSVTSAPTADMATLTVVQPLTLDVVARAIELLEKLOESGEVPHKLSLKI
Db 1 MKPSVTSAPTADMATLTVVQPLTLDVVARAIELLEKLOESGEVPHKLSLKI
Qy 61 FCTAIRVQYMHETITVNGCPEFRARATATKATVAFAAEGSHSHPRVVELPKTI
Db 61 FCTAIRVQYMHETITVNGCPEFRARATATKATVAFAAEGSHSHPRVVELPKTI
Qy 121 NVMGKEQNSPIYISRIITPGVAERHGGKRGDQLLSVNGSVSEGEHHEKAVELI
Db 121 NVMGKEQNSPIYISRIITPGVAERHGGKRGDQLLSVNGSVSEGEHHEKAVELI
Qy 181 SVKLWVRYTPKVLSEMEARFEKLTARRRQOQLLIQQQQQQQQQQQQNQNS
Db 181 SVKLWVRYTPKVLSEMEARFEKLTARRRQOQLLIQQQQQQQQQQQQNQNS

RESULT 2
US-09-370-102-1
; Sequence 1, Application US/09370102
; Patent No. 6265547
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice

15:31:25 2004

us-09-909-005-1.ra1

terson, Chandra
TION: CELL JUNCTION PDZ PROTEIN
: PF-0599 US
ATION NUMBER: US/09/370,102
: DATE: 1999-08-06
ATION NUMBER: 09/151,611
: DATE: 1998-09-11
ID NOS: 3
Program

no sapiens

ATION: 1974337

100.0%; Score 1170; DB 3; Length 233;
larity 100.0%; Pred. No. 2.5e-109;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LVVRYTPKVLMEARPEKLTARRRQQOQLLQQOQQOQQOQQOQQOQQHMS 233
LVVRYTPKVLMEARPEKLTARRRQQOQLLQQOQQOQQOQQOQQOQQHMS 233

lication US/09151611

731

TION:

, Henry

terson, Janice

terson, Chandra

TION: CELL JUNCTION PDZ PROTEIN
: PF-0599 US
ATION NUMBER: US/09/151,611
DATE: 1998-09-11
ID NOS: 3
Program

norhabditis elegans

TION: g1685067

55.0%; Score 643.5; DB 2; Length 297;
larity 70.6%; Pred. No. 2e-56;
Conservative 29; Mismatches 23; Indels 1; Gaps 1;
DVARAIELLEKQESGEVPHKLSKVLQSEFCTAIREVYQVHETITVNGCPEF 84
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ATAKATVAFAASEGHSHPRVVELPKTDEGLGNVNGGKEQNSPIYSRIIPGVAE 144
ATAKATVAFAASEGHSHPRVVELPKTDEGLGNVNGGKEQNSPIYSRIIPGVAE 236
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RESULT 4

US-09-370-102-3
; Sequence 3, Application US/09370102
; Patent No. 6265547
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: CELL JUNCTION PDZ PROTEIN
; FILE REFERENCE: PF-0599 US
; CURRENT APPLICATION NUMBER: US/09/370,102
; CURRENT FILING DATE: 1999-08-06
; EARLIER APPLICATION NUMBER: 09/151,611
; EARLIER FILING DATE: 1998-09-11
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; OTHER INFORMATION: g1685067
US-09-370-102-3

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Best Local Similarity 70.6%; Pred. No. 2e-56;
Matches 127; Conservative 29; Mismatches 23; Indels 1;

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Db 177 KAAATATVAFAASEGHSHPRVVELPKTDEGLGNVNGGKEQNSPIYSRIIP
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Db 237 RHGGLKRGDQLSVNGSVGEHHEKAVELLKAARDVKLVVRYTPKVLMEAR

RESULT 5

US-09-562-737-21
; Sequence 21, Application US/09562737
; Patent No. 6428967
; GENERAL INFORMATION:
; APPLICANT: Herz, Joachim
; APPLICANT: Gotthardt, Michael
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; FILE REFERENCE: UTSW0708
; CURRENT APPLICATION NUMBER: US/09/562,737
; CURRENT FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-562-737-21

Query Match 16.8%; Score 196.5; DB 4; Length 724;
Best Local Similarity 41.4%; Pred. No. 4.5e-11;
Matches 41; Conservative 19; Mismatches 38; Indels 1;

QY 106 PRVVELPKTDEGLGNVNGGKEQNSPIYSRIIPGVAERHGLKRGDQLSVNG

us-09-909-005-1.ra1

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QY 106 PVWELPKTDEGLGFWNGGKEQNSPIYTSRIIPGGVAEBHGELKRGDQLLSVNG
DB 311 PRRIVHRGTTGLGFNIV-GVEDEGIFISWILAGGPADDYGLKRGQDTASVNG
QY 166 EHHEKAVELLKAAKQSVKLAVRYRTPKVLEEMEARPEKLR 204
DB 370 DSHEQAALENAGQVTIIIPQYKPEYSRGEAKIHLR 408

RESULT 10
US-09-080-855-12
; Sequence 12, Application US/09080855A
; Patent No. 6083721
; GENERAL INFORMATION:
; APPLICANT: Saras, Jan
; APPLICANT: Franzn, Petra
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Hellman, Ulf
; APPLICANT: Gonez, Leonel Jorge
; APPLICANT: Heldin, Carl-Henrik
; TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERF
; FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/09/080,855A
; CURRENT FILING DATE: 1998-05-18
; EARLIER APPLICATION NUMBER: 08/805,583
; EARLIER FILING DATE: 1997-02-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 2466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-080-855-12

Query Match 15.4%; Score 180.5; DB 3; Length 2466;
Best Local Similarity 27.9%; Pred. No. 1e-08; Indels 37;
Matches 51; Conservative 31; Mismatches 64;

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DB 1034 PERRKHSDSSSDSDGGQAYVLVDVHKRWISVSSPEREITLVNKKDQYGLGFC
QY 127 EQ---NSPTIYSRIIPGGVAERHGLKRGDQLLSVNGSVSGEHEHKAVELLKAF
DB 1094 KMGRLDGLGFISSVARGGPADFHGCLKPGDRLLSVNSVLSLEGVSHHAAEILQNL
QY 184 LVV 186
DB 1154 LVI 1156

RESULT 11
US-09-566-076-12
; Sequence 12, Application US/09566076
; Patent No. 6475775
; GENERAL INFORMATION:
; APPLICANT: Saras, Jan
; APPLICANT: Franzn, Petra
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Hellman, Ulf
; APPLICANT: Gonez, Leonel Jorge
; APPLICANT: Heldin, Carl-Henrik
; TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERF
; FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/09/566,076
; CURRENT FILING DATE:
; EARLIER APPLICATION NUMBER: 09/080,855
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 39

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; ORGANISM: Artificial Sequence

us-09-909-005-1.rai

Application US/09100804

472
ATION:
GONEZ, LEONEL JORGE
SARAS, JAN
CLAESSON-WELSH, LENA
HELDIN, CARL-HENRIK
ENTION: PRIMARY STRUCTURE AND FUNCTIONAL
ENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
ENTION: TYROSINE PHOSPHATASES
SEQUENCES: 34
ICE ADDRESS:
WOLF, GREENFIELD & SACKS, P.C.
00 ATLANTIC AVENUE
TON
SSACHUSETTS
USA
0
ADABLE FORM:
E: Floppy disk
IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
Patent In Release #1.0, Version #1.25
ICATION DATA:
N NUMBER: US/09/100,804
E:
TION:
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N NUMBER: US 08/596,291
E: 09-AUG-1996
N NUMBER: US 08/115,573
E: 01-SEP-1993
ATION DATA:
N NUMBER: PCT/US94/09943
E: 01-SEP-1994
NT INFORMATION:
ES, EDWARD R.
ON NUMBER: 31,616
DOCKET NUMBER: LO461/7003
ATION INFORMATION:
617-720-3500
617-720-2441

R SEQ ID NO: 16:
RACTERISTICS:
7 amino acids
no acid
SS: single
linear
E: peptide
: NO
NO